

STIC-Biotech/ChemLib

75876

**From:** Chan, Christina  
**Sent:** Tuesday, September 17, 2002 8:22 AM  
**To:** Kemmerer, Elizabeth; STIC-Biotech/ChemLib  
**Subject:** RE: rush seq search req

Please rush. Thanks Chris

Chris Chan  
TC 1600 New Hire Training Coordinator and SPE, 1644  
CM 1, Room 9B19  
308-3973

-----Original Message-----

**From:** Kemmerer, Elizabeth  
**Sent:** Tuesday, September 17, 2002 8:21 AM  
**To:** Chan, Christina  
**Subject:** rush seq search req

Chris-  
Please approve the following rush request for a date case that Bonnie just transferred to me.  
Thanks.

STIC:  
Please rush a search of SEQ ID NO: 69 for 09/944396. Thanks.

Elizabeth (Betsy) Kemmerer  
Art Unit 1646  
308-2673  
CM1-10B17  
Mailbox: 10D19

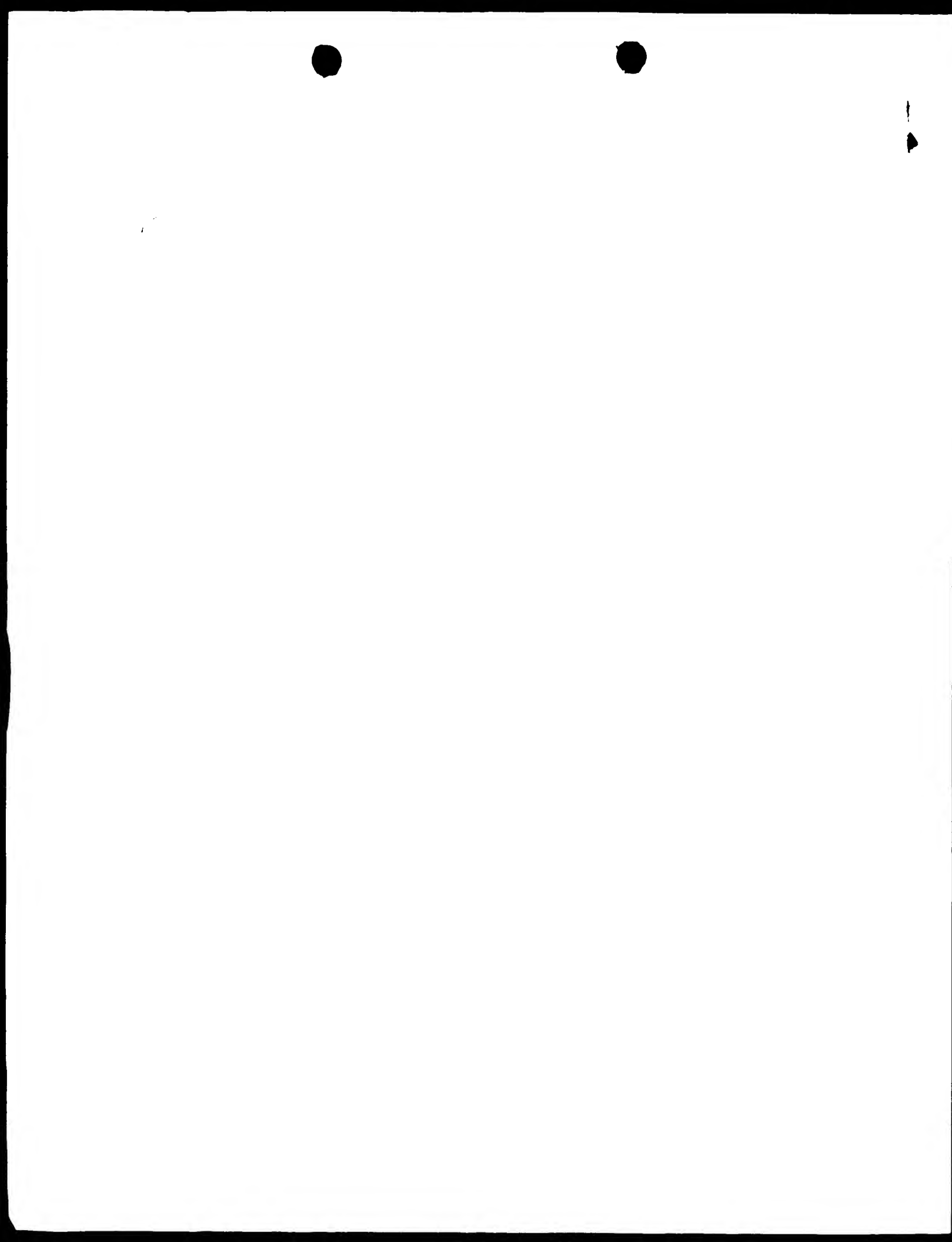
Searcher: P. Schreiber  
Phone: 308-4272  
Location: CM1 6A03  
Date Picked Up: 9/17  
Date Completed: 9/18  
Searcher Prep/Review: 8  
Clerical: \_\_\_\_\_  
Online time: 5

TYPE OF SEARCH:

NA Sequences: \_\_\_\_\_  
AA Sequences: 1  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

VENDOR/COST (where applic.)

STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
Questel/Orbit: \_\_\_\_\_  
DRLink: \_\_\_\_\_  
Lexis/Nexis: \_\_\_\_\_  
Sequence Sys.: CompuLink  
WWW/Internet: \_\_\_\_\_  
Other (specify): \_\_\_\_\_





XX Antibody against proteins expressed in neoplastic cells, useful for  
PI tumor diagnosis and treatment  
XX  
XX  
XX Example 1: Fig 16; 162pp; English.  
XX  
XX This sequence of proteins from the p53 (p53-14) protein encoded  
CC by the novel cDNA clone DNA44804 (see AAX87261). Amplification of  
CC DNA44804 was observed in various tumor lines, especially in colon  
CC tumours, suggesting a role in tumour formation or growth. Antagonists  
CC (e.g. antibodies) directed to p53 may have use in cancer therapy.  
CC The invention identifies 14 genes (see AAX87264-67) that are amplified  
CC in the genome of tumour cells. Such amplification is expected to be  
CC associated with overexpression of the gene product and to contribute  
CC to tumorigenesis. The encoded proteins (see AAX86477-90) may be  
CC useful targets for the diagnosis and/or treatment (including  
CC prevention) of certain cancers, and may act as predictors of the  
CC prognosis of tumour treatment. Antibodies that bind the proteins  
CC are claimed and used in claimed cancer diagnostic kits.  
Sequence 598 AA;

Query Match 100.0%; Score 3135; DB 20; Length 598;  
Best Local Similarity 100.0%; Prod No 20-101;  
Matches 598; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MCSRVLLPLLLLLALGFGVQCCSGGCGSGPVTFTAKGTTVPVGFDTGVLVVF 60  
Db 1 mcsrvllplllllalgpvqpcsgcgsgpvtftarqgtvrvpvdvlglyvf 60  
QY 61 ENGITMELASSAGHLEGLSLMSQVQASLEPFLMLLLASUNLLALPFGILLDAVE 120  
Db 61 enqitmelassaghlglslmsqvaslepfllmlldslunllalpfgilldave 120  
QY 121 ALPAGCGCGQHPGLFSPHFNHLDVSNQGFVWVFWVETKCTPEPIAGNTPAQI 180  
Db 121 alpagcgcgqhpglfshfnhldvsnqglvfwvfwvqtrctpepiagntpaqi 180  
QY 191 PDEPLACVAAQPLVSNLSLZALPGRSGLPGRSGLPGRSGLPGRSGLPGRSGL 240  
Db 191 pdeplacvaaqplvsnlszlalpgrrsgrlpgrrsgrlpgrrsgrlpgrrsgrl 240  
QY 241 CHVLAETPT 300  
Db 241 shvlaspt 300  
QY 301 APTWLSPLATAPSPSTAPVTPVTPVTPVTPVTPVTPVTPVTPVTPVTPVTPV 360  
Db 301 aptwlsplatapspstapvtpvtpvtpvtpvtpvtpvtpvtpvtpvtpvtpv 360  
QY 361 PPTVYSSGAGVTPPT 420  
Db 361 pptvysagvtppt 420  
QY 421 LTPNLSGHEPLVLLPLDASAPYTVTGLRPNATVYCVMLPGHGVHSGEACCAHT 480  
Db 421 ltpnlsghelplvllpldasapytvvtglrpnatvycvmlpghgvhsgacah 480  
QY 481 PPAVSHNAPVTOARGNPLLLIAPALAAVLLAALAAVGAAYCVKRGKMAAAQKQV 540  
Db 481 ppavshnapvtorgnpllllialalaaavlllaalaaavgaaycvkrgrkma 540  
QY 541 GPGAGPLELGVKVPLEPKRATGEGEALPSGSETEVPLMGFGPGGLQSPHAKPYI 598  
Db 541 gpgagplelgvkvplepkratgegealpsgsetevplmgfgpgglqspahaky 598

RESULT 2  
AAY94691  
ID AAY94691 standard; Protein: 598 AA.  
XX  
AC AAY94691;

XX 03-OCT-2000 (first entry)  
XX  
XX Amino acid sequence of novel polypeptide PRO457.  
XX  
XX PRO292; PRO297; PRO298; PRO299; PRO300; PRO301; PRO302; PRO303;  
XX PRO304; PRO305; PRO306; PRO307; PRO308; PRO309; PRO310; PRO311;  
XX tumorigenesis; cancer; neoplastic cell growth; cell proliferation.  
XX Homo sapiens.  
XX Key location/qualifiers  
XX Peptide 1..23  
XX Region 14..25  
XX Note= "Signal sequence"  
XX Modified site 23..29  
XX Note= "N-myristoylation site"  
XX Modified-site 27..33  
XX Note= "N-myristoylation site"  
XX Modified-site 112..118  
XX Note= "N-myristoylation site"  
XX Region 122..144  
XX Note= "leucine zipper"  
XX Region 194..216  
XX Note= "leucine zipper"  
XX Modified-site 198..202  
XX Note= "N-glycosylation site"  
XX Modified-site 262..270  
XX Note= "tyrosine kinase phosphorylation site"  
XX Modified-site 273..279  
XX Note= "N-myristoylation site"  
XX Modified-site 425..429  
XX Note= "N-glycosylation site"  
XX Modified-site 453..457  
XX Note= "N-glycosylation site"  
XX Domain 501..520  
XX Note= "transmembrane domain"  
XX Modified-site 519..525  
XX Note= "N-myristoylation site"  
XX Modified-site 565..571  
XX Note= "N-myristoylation site"  
XX W000003740-A2.  
XX  
XX 29-JUN-2000.  
XX  
XX 16-DEC-1999; 99WO-US30095.  
XX  
XX 22-DEC-1998; 98US-0113296.  
XX 08-MAR-1999; 99WO-US05028.  
XX 02-JUN-1999; 99WO-US05028.  
XX 01-SEP-1999; 99WO-US20111.  
XX 15-SEP-1999; 99WO-US21090.  
XX 30-NOV-1999; 99WO-US28413.  
XX 30-NOV-1999; 99WO-US28499.  
XX 01-DEC-1999; 99WO-US28401.  
XX 02-DEC-1999; 99WO-US28565.  
XX (GENE ) GENENTECH INC.  
XX  
XX Botstein D, Goldard A, Gurney AL, Hillis E, Lawrence LA, Ray MA;  
XX Wood WI;  
XX WPI: 2000-452188/49.  
XX N-PSDB; AAM6922.  
XX  
XX New anti-polypeptide antibody useful in the treatment and diagnosis of  
XX neoplastic cell growth and proliferation -  
XX Claim 61; Fig 16; 220pp; English.  
XX  
XX The present sequence represents a novel human polypeptide. The  
XX





QY 541 GPAGAPLEGVKVPLESPKATEGGREALPSSSECEVPMKSPGPGCLQSPHAKPYI 598  
 DB 541 GPAGAPLEGVKVPLESPKATEGGREALPSSSECEVPMKSPGPGCLQSPHAKPYI 598

RESULT 5  
 AAB07428  
 ID AAB07428 standard; Protein: 673 AA.  
 AC AAB07428.  
 DE 20-OCT-2000 (first entry)  
 XX Amino acid sequence of a leucine-rich surface glycoprotein (LRSg).  
 XX Leucine-rich surface glycoprotein; LRSg.  
 XX Homo sapiens.

Key Location/Qualifiers  
 Peptide 1..23  
 FT Region /note= "signal peptide"  
 FT Region 77..309 /note= "leucine-rich region"  
 FT Region 101..123 /note= "leucine-rich repeat"  
 FT Region 125..147 /note= "leucine-rich repeat"  
 FT Region 149..171 /note= "leucine-rich repeat"  
 FT Region 217..238 /note= "leucine-rich repeat"  
 FT Region 240..263 /note= "leucine-rich repeat"  
 FT Region 289..309 /note= "leucine-rich repeat"  
 FT Domain 409..441 /note= "PCF-like domain"  
 FT Domain 460..535 /note= "fibronectin type III domain"  
 FT Domain 576..599 /note= "transmembrane domain"

W0200042170 A1.  
 20-JUL-2000.  
 21-APR-1999; 99W0508792.  
 21-APR-1998; 98W02063950.  
 (MILL.) MILLENNIUM BIOTHERAPEUTICS INC.  
 Holzman JA;  
 WPI; 2000-422823/42.  
 N-PSDB; AAA58765, AAA58766.  
 New leucine-rich surface glycoprotein (LRSg) polynucleotides and polypeptides used in diagnostics and screening assays to identify modulators used to treat LRSg associated disorders -  
 Claim 9; Fig 1; 139pp; English.  
 The present sequence represents a leucine-rich surface glycoprotein (LRSg). Modulators of LRSg can be used to treat disorders characterized by aberrant LRSg protein or nucleic acid expression or activity. The LRSg proteins can be used to treat disorders associated with insufficient or excessive production of LRSg, or LRSg target molecules. LRSg proteins and antibodies specific for it are used in screening assays, diagnostic assays, prognostic assays for monitoring clinical trials and in pharmacogenetics.

XX Sequence 673 AA;  
 SQ

Query Match 98.4%; Score 3083.5; DB 21; Length 673;  
 Best Local Similarity 88.7%; Pred No. 4.4e-188;  
 Matches 597; Conservative 0; Mismatches 1; Indels 75; Gaps 1;

QY 1 MCSRVPLLDLLDLDLALPGVQVQPSQSQSQVVECTARQCTTVPRDVPDVTGLVYF 60  
 DB 1 MCSRVPLLDLLDLDLALPGVQVQPSQSQSQVVECTARQCTTVPRDVPDVTGLVYF 60  
 QY 61 ENGITMLDASSFAGLQCLQLLDLSQNIAS----- 90  
 DB 61 ENGITMLDASSFAGLQCLQLLDLSQNIAS----- 90  
 QY 62 GRTIMLDASSFAGLQCLQLLDLSQNIAS----- 120  
 DB 62 GRTIMLDASSFAGLQCLQLLDLSQNIAS----- 120  
 QY 91 -----LRPLRLLDLSDHNS 105  
 DB 91 -----LRPLRLLDLSDHNS 105  
 QY 121 RLRIRIYLGKRIIRHQPAATDLDRLLEIKIQDNEIRLPPILRPLLDLSDHNS 180  
 DB 121 RLRIRIYLGKRIIRHQPAATDLDRLLEIKIQDNEIRLPPILRPLLDLSDHNS 180  
 QY 196 LLAIPFCLIPARVIALRACGLQCS DQVPSFANRMLAWSDQGLRVPVIRGLRG 165  
 DB 196 LLAIPFCLIPARVIALRACGLQCS DQVPSFANRMLAWSDQGLRVPVIRGLRG 165  
 QY 191 LLAIPGILDRANQALRAGLQGLDQGLRIRLRLDLDSDQGLRVPVIRGLRG 240  
 DB 191 LLAIPGILDRANQALRAGLQGLDQGLRIRLRLDLDSDQGLRVPVIRGLRG 240  
 QY 140 LTRFLAGRTFAGTSPHETACTAALQPTDVSNGISQATPDHSCLLPPLLLAAARPP 225  
 DB 140 LTRFLAGRTFAGTSPHETACTAALQPTDVSNGISQATPDHSCLLPPLLLAAARPP 225  
 QY 241 LTRFLAGRTFAGTSPHETACTAALQPTDVSNGISQATPDHSCLLPPLLLAAARPP 400  
 DB 241 LTRFLAGRTFAGTSPHETACTAALQPTDVSNGISQATPDHSCLLPPLLLAAARPP 400  
 QY 226 NGVPSWPPWPPESIVLTASPEFCHPPKNAKPIILPIYAPPGTATTIATVPT 285  
 DB 226 NGVPSWPPWPPESIVLTASPEFCHPPKNAKPIILPIYAPPGTATTIATVPT 285  
 QY 201 NGVPSWPPWPPESIVLTASPEFCHPPKNAKPIILPIYAPPGTATTIATVPT 460  
 DB 201 NGVPSWPPWPPESIVLTASPEFCHPPKNAKPIILPIYAPPGTATTIATVPT 460  
 QY 286 TRVVVKEPVAISSSLAVHLSHAPAFPAISPPSTAPPVQVQVQPSQSQSQVVECT 345  
 DB 286 TRVVVKEPVAISSSLAVHLSHAPAFPAISPPSTAPPVQVQVQPSQSQSQVVECT 345  
 QY 362 LTRFLAGRTFAGTSPHETACTAALQPTDVSNGISQATPDHSCLLPPLLLAAARPP 420  
 DB 362 LTRFLAGRTFAGTSPHETACTAALQPTDVSNGISQATPDHSCLLPPLLLAAARPP 420  
 QY 346 HICTRHRLACTCPGPGTGYCFSSQSGQCTPSPPTVPPTPPTSLTISIPVSPSTIS 405  
 DB 346 HICTRHRLACTCPGPGTGYCFSSQSGQCTPSPPTVPPTPPTSLTISIPVSPSTIS 405  
 QY 421 HICTRHRLACTCPGPGTGYCFSSQSGQCTPSPPTVPPTPPTSLTISIPVSPSTIS 480  
 DB 421 HICTRHRLACTCPGPGTGYCFSSQSGQCTPSPPTVPPTPPTSLTISIPVSPSTIS 480  
 QY 405 QPYLQSSSVLPSPPIYPPHSGTQKPVVILPILASGLAPYVQLKRAIYSCVMPHGP 465  
 DB 405 QPYLQSSSVLPSPPIYPPHSGTQKPVVILPILASGLAPYVQLKRAIYSCVMPHGP 465  
 QY 491 QPYLQSSSVLPSPPIYPPHSGTQKPVVILPILASGLAPYVQLKRAIYSCVMPHGP 540  
 DB 491 QPYLQSSSVLPSPPIYPPHSGTQKPVVILPILASGLAPYVQLKRAIYSCVMPHGP 540  
 QY 466 GAVTQGLANLALHICPAVHSHAPVTCARNGCLPLILALAAVLAALAAVAAVGVK 525  
 DB 466 GAVTQGLANLALHICPAVHSHAPVTCARNGCLPLILALAAVLAALAAVAAVGVK 525  
 QY 541 GAVTQGLANLALHICPAVHSHAPVTCARNGCLPLILALAAVLAALAAVAAVGVK 600  
 DB 541 GAVTQGLANLALHICPAVHSHAPVTCARNGCLPLILALAAVLAALAAVAAVGVK 600  
 QY 536 PTPAMAAAGTQGVVPMAGPPIETPVVVIIPSPVATPQVPAIDSPSPVPIIMGRG 585  
 DB 536 PTPAMAAAGTQGVVPMAGPPIETPVVVIIPSPVATPQVPAIDSPSPVPIIMGRG 585  
 QY 661 PTPAMAAAGTQGVVPMAGPPIETPVVVIIPSPVATPQVPAIDSPSPVPIIMGRG 660  
 DB 661 PTPAMAAAGTQGVVPMAGPPIETPVVVIIPSPVATPQVPAIDSPSPVPIIMGRG 660  
 QY 586 PGLQSPHAKPYI 598  
 DB 586 PGLQSPHAKPYI 598  
 QY 661 PGLQSPHAKPYI 673  
 DB 661 PGLQSPHAKPYI 673

RESULT 6  
 AAB87543  
 ID AAB87543 standard; Protein: 673 AA  
 AC AAB87543;  
 DE 15-MAY-2001 (first entry)  
 XX Human PR-1282.  
 XX Human; PR-1282; mapping.  
 XX Homo sapiens.  
 XX W0200116318-A2.  
 XX





PI Ashkenazi AJ, Baker KF, Bolstein D, Desnoyers L, Eaton SL,  
 PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ,  
 PI Grimaldi CL, Harney AL, Johnson D, Majer MA, Pao L, Pao L, R,  
 PI Roy MA, Stewart TA, Tamas D, Watanabe CK, Williams PM, Wood WJ,  
 PI Zhang Z.  
 XX WFL: 2561-2573 (13)  
 DE N-PSDB: AAF44105.  
 XX PRO polynucleotides used to produce polypeptides used to target  
 PT bioactive molecules such as toxins, radiolabels or antibodies, to  
 PT specific cells, to cause targeted cell death -  
 XX  
 XX Claim 12: Fig 32; 935pp; English.

XX The present invention describes human secreted and transmembrane p90  
 CC proteins. The p90 proteins have cytosolic activity. The p90 proteins  
 CC can be used for targeted delivery of bioactive molecules, such as  
 CC toxins, radiolabels or antibodies, that cause cell death. p90 nucleotide  
 CC sequences, and their fragments, can be used as hybridisation probes, in  
 CC chromosomal and gene mapping, and in the generation of anti-sense RNA  
 CC and cDNA. They may also be used to produce transgenic animals which are  
 CC used to develop and screen therapeutically useful reagents. The p90  
 CC nucleotide and protein sequence can be used for tissue typing and in  
 CC treating cancer. Anti-p90 antibodies can be used in diagnostic assays.  
 CC AAF44270 to AAF44473 represent PCR primers and hybridisation probes used  
 CC in the isolation of human p90 sequences. AAF44087 to AAF44265 and  
 CC AAF65154 to AAF65303 represent human p90 polynucleotide and protein  
 CC sequences given in the exemplification of the present invention.

XX Sequence 673 AA:

Query Match 98 48; Score 3084.5; WR 22; Length 673;  
 Best Local Similarity 88 74; Seed No 4 40-188;  
 Matches 597; Conservative 0; Mismatches 1; Indels 75; Gaps 1;  
 QY 1 MCSRVLELLPILLALLAEGWVWSPSSSTQVSPQVIVTAPQVIVVWPPVIVVWVVF 60  
 Db 1 mcsrvpvlip:lllaaegv:llpsaqsqspqvtatctatqgtvtdrpfk:Ragyl:1 60  
 QY 61 ENGITMIDASSFAGIPGQILDMUNQIAS----- 90  
 Db 61 engitmidassfaqipgqildmunaqiaspsavtqlpaulsldlranrlheltnet:1 120  
 QY 91 -----LRLPRLLLLDLSHNS 105  
 Db 121 rqlrrierlylqknrlrhqpaqtdtldrlleklqdelralpprlprllldshns 180  
 QY 106 LLALFPGIITDANVETRIAGIQLQQLDEGLFSRLRLHLDVSDNQLERVPVIRGLRG 165  
 Db 101 llaaegvllldssaaal:laag:llpdeg:fsrlrnlhldvsdnqlervpv:ragyl:1 240  
 QY 166 ITRIRIANTRIADLPEDLACLAALQELVSNLSIALQEDLSGLPPELELLAAANPF 225  
 Db 241 ltririlauntlrlqpedlqlaqlqelvdvsnlsqalqpdlsqllprlllaaanpl 300  
 QY 226 NCWCPLSWPGVWRESHVITLSPETRCCHPDKVAGHLLLELDYADGSCPAFTTATVPT 285  
 Db 301 ncwcp:lsfwvreshv:tlasp:etrcchpdkvaghllleldyadgscpaftttatvpt 450  
 QY 286 TRPVVREPTA.LSSSLAPTMLSPATATAPSPPTAPTPVGPVGFQDMCPSTCLNGGTC 345  
 Db 361 trpvv:repta:lssslaptmlspatatapsppstaptpv:gpv:gfqdmcpstclngg:tc 420  
 QY 346 HLCETHILACVCPGFTGIVGYSQMGQTPSPPTWTTPRPSPSLTIGIEVVSISLVGL 405  
 Db 421 hlcethilacvcp:ftgivgysqmgqtpspptwttp:rp:sp:slt:igievvsislvgl 480  
 QY 406 QVVLQSSVQLPSLRI TYPNRI SGDKPKLVLTLLRLPASIAEYTVTLPPNATYSVCMPLGP 465  
 Db 481 qvvlqssvqlpslrl:typnri:sgdkpklvltllrl:pasiaeytv:tlppnatysvcmplgp 540

QY 456 GRVINGELACSEAHFPAVILNHMFVTCASGHEFELLIAPALAAVILALAAVCAAYVR 525  
 Db 541 grvingelacseahfpa:vilnhmfvtcasghefel:liapalaa:vilalaa:vcayvr 600  
 QY 526 KSRAMAAALFQVAVSAGVAFVLEFEGVAVVLEFVFAFEGGSEALFSGSDEVPFLMFPFG 585  
 Db 601 ksr:amaaalfqvav:sa:gvafvle:fegvavvle:fvfafeggs:ea:lfsgsdevpflmfpfg 660  
 QY 586 PGIASPLHAKPYI 598  
 Db 661 pgiasplhakyi 673  
 RESULT 8  
 AAB84689  
 ID AAB84689 Standard, Protein: 673 AA.  
 AC AAB84689;  
 XX  
 XX 17-SEP-2001 (first entry)  
 XX Amino acid sequence of human slit polypeptide 25113.  
 XX Slit protein, zslit3; neurite growth; cellular proliferation;  
 XX immune response; stroke; brain damage; paralysis; Huntington's disease;  
 KW neurodegenerative disease; amyotrophic lateral sclerosis;  
 KW Alzheimer's disease; Parkinson's disease; peripheral neuropathy;  
 KW demyelinating disease; multiple sclerosis; lung organogenesis;  
 KW pulmonary disease; respiratory circulation; cystic fibrosis; asthma;  
 KW immunosuppression; autoimmune disease; insulin-dependent diabetes;  
 KW rheumatoid arthritis.  
 XX  
 OS Homo sapiens.  
 XX  
 XX Location/Qualifiers  
 FT Peptide 1..23 /note="signal peptide"  
 FT Protein 24..650 /note="mature protein"  
 FT Domain 53..287 /note="LRR domain comprising LRR motifs"  
 FT Modified-site 101 /note="N-linked glycosylation site"  
 FT Modified-site 117 /note="N-linked glycosylation site"  
 FT Modified-site 273 /note="N-linked glycosylation site"  
 FT Modified-site 304 /note="N-linked glycosylation site"  
 FT Domain 409..441 /note="EGF domain"  
 FT Modified-site 420 /note="putative prenylation site"  
 FT Modified-site 500 /note="N-linked glycosylation site"  
 FT Modified-site 528 /note="N-linked glycosylation site"  
 FT Modified-site 534 /note="putative prenylation site"  
 XX W0200146418:AL.  
 XX 28-JUN-2001.  
 XX 14-DEC-2000; 2000WO-US34230.  
 XX 21-DEC-1999; 99US-0469847.  
 XX (ZYMO) ZYMOGENETICS INC.  
 XX Holloway JL, Chandrasekhar YA;  
 XX WPI: 2001-441677/47.









Domain	577..600	
FT	/note "transmembrane domain."	
XX		
PN	W0209042170-A1.	
XX		
PD	20-JUL 2009.	
XX		
PF	21-APR-1999; G0W0-0568792	
PP		
PP	21-APR 1998; G0NS-0573950	
XX		
XX	(MILL-) MILLENNIUM BIOTHERAPEUTICS INC.	
XX		
DI	Holtzman DA;	
DR	WPI; 2000-482823/42.	
DR	N-PSDB; AAA58767.	
PT	New leucine-rich surface glycoprotein (LPSG) polypeptides and	
PT	polypeptides used in diagnostics and screening assays to identify	
PT	modulators used to treat LPSG associated disorders -	
XX		
XX	Claim 9; Fig 3; 139pp; English.	
XX		
CC	The present sequence represents a leucine rich surface glycoprotein	
CC	(LPSG). Modulators of LPSG can be used to treat disorders	
CC	characterized by aberrant LPSG protein or nucleic acid expression	
CC	or activity. The LPSG proteins can be used to treat disorders	
CC	associated with insufficient or excessive production of LPSG, or	
CC	LPSG target molecules. LPSG proteins and antibodies specific for	
CC	LPSG are used in screening assays, diagnostic assays, prognostic	
CC	assays for monitoring clinical trials and in pharmacogenetics.	
XX		
SQ	Sequence 493 AA;	
XX		
Query Match	53.3%; Score 1672; DB 21; Length 493;	
Best local Similarity	53.3%; Prod No. 1.8e-98;	
Matches 356;	Conservative 14; Mismatches 40; Indels 258; Gaps	
QY	6 PLIPPLILLALGPVGGPSSGQSSQGVIVHAKWCHVPPVAPVGVWGLVVPNGH 65	
Db		
9 p11--     vllvg 66		
QY	66 MIFASSPACVETQLEKSONQAS----- 99	
Db		
67 TLVAGCALPGLALDISGQSLSPGLGPGVIGPVLNLSADLTKALHLSNCTFLGHT 126		
QY	67 -----LPPLPILLIDISNLSALP 110	
Db	127 LeryLp 106	
QY	111 PGILDTANVEALPLANLTAQVDMNLESPKMLHJWSINQLKPVPPVPLPSGLPPL 170	
Db		
187 PGLTANVEALPLGL 246		
QY	171 LAGNTRIAGLPFPIAGLAAIPELVINLSGALPDELSEGLPPLPLAARNPENCVP 230	
Db		
247 LAGNTRIAGLPDELGLALGLGLGLGLGLGLGLGLGLGLGLGLGLGLGLGLGL 306		
QY	231 LSWIPLVWPTVSHVTLASPPKPRFPRFPRKNAQPLLTPIYALFQGLATTATVPTFTW 290	
Db		
307 LSWIPLVWPTVSHVTLASPPKPRFPRFPRKNAQPLLTPIYALFQGLATTATVPTFTW 330		
QY	291 REPTALNSSTAPTWLSPATAPASPSPSTAPPTVGPVGPQCPSPSTCLNGTCLGP 350	
Db	331 ----- 330	
QY	351 HHVAGLPDEGTHLYPESQWGLTPESTPEVTPPEPESLILSLTEPVPISLWGLAYLQ 410	
Db	331 ----- 330	
QY	411 TSSVAGLNSLPIYENLNGEKWVLEHLEPASTATVTVGLPPRAVLSVWVPLGGPVPF 470	







Db 419 hflkhltpgadydclcllaefaaagpsdltatrlilgcabfstlpasplcha!qahvlqgt 478  
Qy 499 LPLLIAPALAAVLLAALAAVGAAYCVRGRAMAAAOQKGOVGFAGACPLEGVK 553  
Db 476 hv...avgtlqaativftvaillv rgrg ...aguglflklshq 518

Search completed: September 17, 2002, 09:51:20  
Job time: 1837 sec







```

1  APPLICANT: Ron, Dorit
2  TITLE OF INVENTION: WD-49 - Derived peptides and Uses
3  TITLE OF INVENTION: Theof
4  NUMBER OF SEQUENCES: 255
5  CORRESPONDENCE ADDRESS:
6  ADDRESSEE: Morrison & Foerster
7  STREET: 2000 Pennsylvania Avenue, NW
8  CITY: Washington
9  STATE: DC
10 COUNTRY: USA
11 ZIP: 20006-1812
12 COMPUTER READABLE FORM:
13 MEDIUM TYPE: floppy disk
14 COMPUTER: IBM PC compatible
15 OPERATING SYSTEM: PC-DOS/MS-DOS
16 SOFTWARE: Patent Release #1.0, Version #1.25
17 CURRENT APPLICATION NUMBER: US 09/477,346
18 FILING DATE: 07-JUN-1995
19 CLASSIFICATION: 514
20 PRIOR APPLICATION DATA:
21 APPLICATION NUMBER: 09/487,072
22 FILING DATE: 07-JUN-1995
23 ATTORNEY/AGENT INFORMATION:
24 NAME: MURASHIGE, KATE H.
25 REGISTRATION NUMBER: 24,979
26 REFERENCE/INVENT NUMBER: 255-325,20
27 TELECOMMUNICATION INFORMATION:
28 TELEPHONE: (202) 887-1500
29 TELEFAX: (202) 887-0763
30 INFORMATION FOR SEQ ID NO: 49:
31 SEQUENCE CHARACTERISTICS:
32 LENGTH: 605 amino acids
33 TYPE: amino acid
34 TOPOLOGY: unknown
35 MOLECULE TYPE: protein
36 HYPOTHEICAL: NO
37 ANTI-SENSE: NO
38 ORIGINAL SOURCE:
39 INDIVIDUAL ISOLATE: Insulin like growth factor binding
40 INDIVIDUAL ISOLATE: protein complex, Flg. 32
41 US-08-477-446-49

```

```

Query Match          9 68: Score 302, DB 4: Length 605;
Best Local Similarity 25.58; Prod. No. 5.4e-14;
Matches 98, Conservative 40, Mismatches 58, Gaps 11;

7  LLLPLLL--LALG-----PGVQG-----GPSGCGCSQPO-----IVFTARQGIT 45
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 8  LALALLLSWVAIGPRPSLEGADPTGEGAEAPAPACACVSYDDADHLSVFCSSNLT 67

46  VPRVPPPTVGLVYFENGITMDASSFAGLPGGLDLSQNTASLRLLPRLLL----- 98
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 68  LPDVGPGTQALWLDGNNISVVVAAAFQNISSLCFTNLRQZQGLSLR  PVALGLGNLICH 126

99  LILSHNSLLALEPGILDTANVAEALPLAGLG---LQOI DEGI FSPRLNHLIDVSDQLEP 155
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 127  LHLERNQLPSALGTF--AHTPALASLGSSNNPLSRLEDGLFEGIGSLMDNLGNWSLAV 184

156  VP-PVIRGLRGLRLRAGNTRFAGI RPDIAAGI AALQELDVSNLSIGALPGHLSLFLPR 214
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 185  LPDAAFPGIGSRGLRGLVAGN-RLAYLQALPLFSGIAELRELDLSKNALRAIKANVFFVQLPR 243

215  LRLAAARNPVNCVPLSWFG-----PWVRESHVTLA 246
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 244  LRLYLDLRLNLAANVAPGAFGLKALPWLIDLSHNEVA 279

```

```

RESULT 5
US-08-477-446-49
; Sequence 49, Application: US/08473089
; Patent No. 6342368

```

```

1  GENERAL INFORMATION:
2  APPLICANT: Mechtly-Rosen, Daria
3  APPLICANT: Ron, Dorit
4  TITLE OF INVENTION: WD 49 - Derived peptides and Uses
5  TITLE OF INVENTION: Theof
6  NUMBER OF SEQUENCES: 265
7  CORRESPONDENCE ADDRESS:
8  ADDRESSEE: Morrison & Foerster
9  STREET: 2000 Pennsylvania Avenue, NW
10 CITY: Washington
11 STATE: DC
12 COUNTRY: USA
13 ZIP: 20006-1812
14 COMPUTER READABLE FORM:
15 MEDIUM TYPE: floppy disk
16 COMPUTER: IBM PC compatible
17 OPERATING SYSTEM: PC-DOS/MS-DOS
18 SOFTWARE: Patent Release #1.0, Version #1.25
19 CURRENT APPLICATION DATA:
20 APPLICATION NUMBER: 09/487,473,089
21 FILING DATE: 07-JUN-1995
22 CLASSIFICATION: 435
23 ATTORNEY/AGENT INFORMATION:
24 NAME: MURASHIGE, KATE H.
25 REGISTRATION NUMBER: 29,959
26 REFERENCE/INVENT NUMBER: 255-325,22
27 TELECOMMUNICATION INFORMATION:
28 TELEPHONE: (202) 887-1500
29 TELEFAX: (202) 887-0763
30 INFORMATION FOR SEQ ID NO: 49:
31 SEQUENCE CHARACTERISTICS:
32 LENGTH: 605 amino acids
33 TYPE: amino acid
34 TOPOLOGY: unknown
35 MOLECULE TYPE: protein
36 HYPOTHEICAL: NO
37 ANTI-SENSE: NO
38 ORIGINAL SOURCE:
39 INDIVIDUAL ISOLATE: Insulin like growth factor binding
40 INDIVIDUAL ISOLATE: protein complex, Flg. 32
41 US-08-473-089-49

```

```

Query Match          9 68: Score 302, DB 4: Length 605;
Best Local Similarity 25.58; Prod. No. 5.4e-14;
Matches 98, Conservative 40, Mismatches 58, Gaps 11;

7  LLLPLLL--LALG-----PGVQG-----GPSGCGCSQPO-----IVFTARQGIT 45
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 8  LALALLLSWVAIGPRPSLEGADPTGEGAEAPAPACACVSYDDADHLSVFCSSNLT 67

46  VPRVPPPTVGLVYFENGITMDASSFAGLPGGLDLSQNTASLRLLPRLLL----- 98
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 68  LPDVGPGTQALWLDGNNISVVVAAAFQNISSLCFTNLRQZQGLSLR  PVALGLGNLICH 126

99  LILSHNSLLALEPGILDTANVAEALPLAGLG---LQOI DEGI FSPRLNHLIDVSDQLEP 155
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 127  LHLERNQLPSALGTF--AHTPALASLGSSNNPLSRLEDGLFEGIGSLMDNLGNWSLAV 184

156  VP-PVIRGLRGLRLRAGNTRFAGI RPDIAAGI AALQELDVSNLSIGALPGHLSLFLPR 214
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 185  LPDAAFPGIGSRGLRGLVAGN-RLAYLQALPLFSGIAELRELDLSKNALRAIKANVFFVQLPR 243

215  LRLAAARNPVNCVPLSWFG-----PWVRESHVTLA 246
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 244  LRLYLDLRLNLAANVAPGAFGLKALPWLIDLSHNEVA 279

```

```

RESULT 6
US-09-188-930-305
; Sequence 305, Application: US/09188940A
; Patent No. 6350502
; GENERAL INFORMATION:

```

1 APPLICANT: Watson, James D.  
 2 APPLICANT: Strachan, Lorna  
 3 APPLICANT: Sleeman, Matthew  
 4 APPLICANT: Onrust, Rene  
 5 APPLICANT: Murlison, James Greg  
 6 TITLE OF INVENTION: Compositions Isolated From Skin Cells  
 7 TITLE OF INVENTION: and Methods For Their Use  
 8 FILE REFERENCE: 11000.1011c1  
 9 CURRENT APPLICATION NUMBER: US/09/188,930A  
 10 CURRENT FILING DATE: 1998-11-09  
 11 NUMBER OF SEQ ID NOS: 348  
 12 SOFTWARE: FASTSEQ for Windows Version 3.0  
 13 SEQ ID NO 405  
 14 LENGTH: 649  
 15 TYPE: PRT  
 16 ORGANISM: Mouse  
 17 US-09-188-930-305

Query Match 9.5%; Score 298.5; DB 4; Length 649;  
 Best local Similarity 22.8%; Pred. No. 1,10-13;  
 Matches 141; Conservative 80; Mismatches 220; Indels 177; Gaps 23,  
 QY 22 GQPSDQCSQGPVPTVETAKGCTVTVKVPVPTVGLY- ..... 58  
 Db 26 KQSPVPSQVQVYVHPTSTVPTVETATVYQDP-TRVGVTHSEKLEKVE 87  
 QY 59 -----VFENGITMLDASSFAGIPGQIIDLSONQIASLRPP 95  
 Db 88 IYHRSLSLEPTNLFYVNVHFGNNITSTTSSSFPILEELHLEKNSAVSTEE 147  
 QY 96 -----LILLDSHNSLLALEPGIIOIANVEALRLAG----- 126  
 Db 148 GAFKUSNYLRLFLSRNHLSTTPGRLPT--TEFLPDPNRTSTSSPSLHGLTSKPLV 205  
 QY 127 -- --LCLQQLDELESRLNHLIVSNQIPEPPVPIPELPGITPLPLACNTPRIAGLP 181  
 Db 206 LQGNLNNHGIGQKVFNVNITELSLVENSUTAAPVNLPG-TSLERKLYLQDN-HINRVP 263  
 QY 182 PEMAGIAALQFIVNSISGALPDLSCLEPELELLAAAPNPVNGVPLSWFQHWVES 241  
 Db 264 PRASFLRGLFLMSNRNLSLEQFLELDNITETILERNQVYQKMKWVLEKQSL 323  
 QY 242 HVTLASFFPTCHQPKNAQPIIIFIDVAPNCPATTTTATVPTPPVVPPEPTALSSSLA 301  
 Db 424 PVKV-NVRHIM-CAPEKVMMAIKLSAELECKDSGIVSTIQIT-----TAT----- 370  
 QY 402 PTWLSPTAPATEAPSPSTAPTVG--PVP---QPDQPPSTCLNGCHLGRHLACL 356  
 Db 471 -----PNTAYAGQGMVAPVTKQPKTKPKLIKD----- 399  
 QY 457 QPEFETGLCESOMGGTRESPTVPTFRKSLILGIEFVSPTSRLVSLGRYLQSSVQL 416  
 Db 400 -----QRTGSPS-----PKTILITKSVTPVTHHSRLALPMTALRL 438  
 QY 417 KSLRLIYRNLSGP-DKRLVTLKRLPASLAYIVTQLRPNATYSVCMPLGPKGVPEGE-- 473  
 Db 439 SWLKIGHSFAFGSLITETIVT-----GERSEYLVTALEPESPRVCMVPMETSNLYLDET 494  
 QY 474 ACCEHAIPIPAVSHNAVPT--GAFS-----GNLPL--LIAPALAAVLAAALAAVCAAY 522  
 Db 495 VCIETQATPLRMVN--QTTINPEQKPKYKPNPLPLAATIGGAVALVSTALLALV-CWY 551  
 QY 523 CVRGRAMAA-AAQDKGQ 539  
 Db 552 VIKNGSLFSKNCAYSKGR 569

RESULT 7  
 US-08 190 802A-50  
 : Sequence 50, Application US/09/188902A  
 : Patent No. 5519003  
 : GENERAL INFORMATION:

1 APPLICANT: Mochly-Rosen, Daria  
 2 APPLICANT: Ron, Dorit  
 3 TITLE OF INVENTION: WD-40 - Derived Peptides and Uses  
 4 TITLE OF INVENTION: Thereof  
 5 NUMBER OF SEQUENCES: 265  
 6 CORRESPONDENCE ADDRESS:  
 7 ADDRESSEE: Dehlinger & Associates  
 8 STREET: P.O. Box 60850  
 9 CITY: Palo Alto  
 10 STATE: CA  
 11 COUNTRY: USA  
 12 ZIP: 94306-0850  
 13 COMPUTER READABLE FORM:  
 14 MEDIUM TYPE: Floppy disk  
 15 COMPUTER: IBM PC compatible  
 16 OPERATING SYSTEM: PC-DOS/MS-DOS  
 17 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 18 CURRENT APPLICATION DATA:  
 19 APPLICATION NUMBER: US/08/190,802A  
 20 FILING DATE: 01-FEB-1994  
 21 CLASSIFICATION: 530  
 22 ATTORNEY/AGENT INFORMATION:  
 23 NAME: Fabian, Gary R.  
 24 REGISTRATION NUMBER: 33,875  
 25 REFERENCE/DOCKET NUMBER: 8600-0139  
 26 TELECOMMUNICATION INFORMATION:  
 27 TELEPHONE: (415) 324-0880  
 28 TELEFAX: (415) 324-0960  
 29 INFORMATION FOR SEQ ID NO: 50:  
 30 SEQUENCE CHARACTERISTICS:  
 31 LENGTH: 603 amino acids  
 32 TYPE: amino acid  
 33 TOPOLOGY: unknown  
 34 MOLECULE TYPE: protein  
 35 HYPOTHETICAL: NO  
 36 ANTI-SENSE: NO  
 37 ORIGINAL SOURCE:  
 38 INDIVIDUAL ISOLATE: Insulin-like growth factor bind.  
 39 INDIVIDUAL ISOLATE: pro. complex-rat, Fig. 33  
 40 US-08-190 802A-50

Query Match 9.0%; Score 281.5; DB 1; Length 603;  
 Best local Similarity 32.4%; Pred. No. 1,66-127;  
 Matches 92; Conservative 49; Mismatches 106; Indels 47; Gaps 11;

QY 6 PLLIPILL-LALGP-GVGG-----GFSKQCSQPO-----TVETAKGCTT 45  
 Db 8 PALVILLATFVALGPHCHLOGTDFGASIAEGQCPVACTSHDGTDELSTVFSKKNLTH 67  
 QY 46 VPRDVPDPTVRIYVFPFNGITMLDASSFAGIPGQIIDLSONQIASLR-----LPRILL 99  
 Db 68 LPHDTPVSPALWIDGNNISSTPSAAPLNISSLPINIGSWIPLSPGALGQNIYYI 127  
 QY 100 DLSHRSLLALEPGIIL-DTANVEALKLAGLGGLESRLNHLIVSNQIPEPPVPIPELPGITPLPLACNTPRIAGLP- 157  
 Db 128 HLEPNPLRNLAWSLETHETPSLASLSSNLLGPEFELFGLSHLMDLNGWNSLVLPD 187  
 QY 158 PVTWICRGTPTPTATNTRTAGIPEPTAGIAAGTGTAVSNI STGALNGCSLSPURKL 217  
 Db 188 TVPQGLGNLHELVLAGN-KLITYLQALFGLGGLLEFELDLSNALSQVKNVFIHLPIQR 246  
 QY 218 LAARNPNCVPLSWFG----PWVRESIVHLAS-PEETRCHEFP 256  
 Db 247 LYLDRLNLTAVAGAFGLGKMLRWLDLSHNRVAGLMEDF---FP 287

RESULT 8  
 US-08-477-346-50  
 : Sequence 50, Application US/0847746  
 : Patent No. 626203  
 : GENERAL INFORMATION:  
 : APPLICANT: Mochly-Rosen, Daria









```

QY 314 -----AFSPSTAPPTVGPV---PQDQPPSTCGTCHLCTR 360
Db 337 TTPPPWPNFTLHMESITFSKTPSTTEPTISSEPVPEPAPNMTHTEPTP-----390
QY 351 HMLACLPFGTGLACESQMGCTRPSTPTVPPEPESITIGTFP---VSPSTSEVHIGP 407
Db 391 ---SPTTPE-----PTSEPAESPPTPTPTPTIATSPTHIASATSLITPKST 435
QY 408 YLGSS--VQISRLTYENISGPKPLVTLR--LPASLAFTVTLPPNATYSVCMPL 463
Db 436 ETTTIVWVLEETRETFDTGQPKTPTVQCHIFSEFNP PETHES---PPTTIFI 489
QY 464 G-----PGRV-PESEKACGEAHITPPAVISNHAFVTAQEGNLP 500
Db 490 GFYVIGLEFWLIFASVLLILLSWGHVKPQALDSQGAALITATQTHIFLQGRQVTP 549
QY 501 ---LLI---APALAAVILAAIAAAGAAVCVRGKAMAAAQIKGQ 539
550 PAMILFIPQSTPTPSSSIFIVVPPNCPVCPVAGPPPSALSQCPQ 595

RESULT 14
US-08-135-929A-11
: Sequence 11, Application US/08135929A
: Patent No. 5593959
: GENERAL INFORMATION:
: APPLICANT: Miller, Jonathan I.
: APPLICANT: Cunningham, David
: APPLICANT: Lyle, Vicki A.
: APPLICANT: Finch, Clara N.
: APPLICANT: Pincus, Matthew R.
: TITLE OF INVENTION: Mutations in the Gene Encoding the Alpha
: TITLE OF INVENTION: Chain of Platelet Glycoprotein Ib
: NUMBER OF SEQUENCES: 11
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Nixon, Hargrave, Devans & Doyle
: STREET: Clinton Square, P.O. Box 1051
: CITY: Rochester
: STATE: New York
: COUNTRY: USA
: ZIP: 14603
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent in Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/135,929A
: FILING DATE: 14-OCT-1993
: CLASSIFICATION: 514
: ATTORNEY/AGENT INFORMATION:
: NAME: Timian, Susan J.
: REGISTRATION NUMBER: 34,103
: REFERENCE/POCKET NUMBER: 26584/23
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (716) 263-1636
: TELEFAX: (716) 263-1600
: TELEX: 978450
: INFORMATION FOR SEQ ID NO. 11.
: SEQUENCE CHARACTERISTICS:
: LENGTH: 610 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
US-08-135-929A-11

```

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Query Match: 8 38: Score 259; DB 1: Length 610;
Best Local Similarity 24.14; Pred. No. 6.7e-11;
Matches 146; Conservative 230; Mismatches 230; Inpts 188; Gaps 28.
QY 28 CQCSQPT---VECTARQTTVPDVPPTVGLVFFEN-----GITMLDAS 70

```

```

Db 4 CEVSKVASHLEWVCKFPNLIATPPLPKDTTILHISENLVTFESLTIATIMPTRELTQNLND 63
QY 71 SF-----AGLPQLQLDLDSQNGIASL-----KLPLLILLDLSHSLALALRPHILDTA 117
Db 64 RCELRKIVADGTPPLVLTIDLSHNGIQSEPTFGOTLEFALTVDVSNRSLTPIAG-----118
QY 118 NVEALPLACLGLOQLDEGLFSPIPNLHPLVSNQCEPVPD-VIWCIGLITRLQVAGNTR 176
Db 119 ---ALR---GLG-----ELQELYKVNELKTLPPGILLITPKIKRISIA-NNN 159
QY 177 TAC EFTETAYLAAIQEIVKHSICALPTTTC TPTSEFLTAAARHPTTWVTSWMP 234
Db 160 LLELVGLINGLGNLTLLIQFNSTLYTPKGFPSHLIPPAFIHQ---NWLONVFIHYE 216
QY 235 GHWVYES-----HYTLASPTTPTP-----HEDKNAQPLILP--LDYA 270
Db 217 PFWLQUNAFNVYVWKQGVIVAKAMISNVAQVQUNSKRFPVYKYCKKSPITGPKRTIDY 276
QY 271 DFGCPATTTATVPTTPPVPEP-----TALSSSLAPTWLSPTAPATE-- 313
Db 277 DYPPEETEGUKVPATKIVVFEPTKZAHITLFWELFYSNSTASIDSMPSSTPTTGPSTFQ 336
QY 314 -----APSPSTAPPTVGPV---PQDQPPSTCGTCHLCTR 350
Db 337 TTPPPWPNFTLHMESITFSKTPSTTEPTISSEPVPEPAPNMTHTEPTP-----390
QY 351 HMLACLPFGTGLACESQMGCTRPSTPTVPPEPESITIGTFP---VSPSTSEVHIGP 407
Db 391 ---SPTTPE-----PTSEPAESPPTPTPTPTIATSPTHIASATSLITPKST 445
QY 408 YLGSS--VQISRLTYENISGPKPLVTLR--LPASLAFTVTLPPNATYSVCMPL 463
Db 436 ETTTIVWVLEETRETFDTGQPKTPTVQCHIFSEFNP PETHES---PPTTIFI 489
QY 464 G-----PGRV-PESEKACGEAHITPPAVISNHAFVTAQEGNLP 500
Db 490 GFYVIGLEFWLIFASVLLILLSWGHVKPQALDSQGAALITATQTHIFLQGRQVTP 549
QY 501 ---LLI---APALAAVILAAIAAAGAAVCVRGKAMAAAQIKGQ 539
Db 550 PAMILFIPQSTPTPSSSIFIVVPPNCPVCPVAGPPPSALSQCPQ 595

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RESULT 14
US-08-234-265A-11
: Sequence 11, Application US/08234265A
: Patent No. 5624817
: GENERAL INFORMATION:
: APPLICANT: Miller, Jonathan I.
: APPLICANT: Cunningham, David
: APPLICANT: Lyle, Vicki A.
: APPLICANT: Finch, Clara N.
: APPLICANT: Pincus, Matthew R.
: TITLE OF INVENTION: Mutations in the Gene Encoding the
: TITLE OF INVENTION: Chain of Platelet Glycoprotein Ib
: NUMBER OF SEQUENCES: 11
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Nixon, Hargrave, Devans & Doyle
: STREET: Clinton Square, P.O. Box 1051
: CITY: Rochester
: STATE: New York
: COUNTRY: USA
: ZIP: 14603
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent in Release #1.0, Version #1 25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/234,265A
: FILING DATE: 28-APR-1994
: CLASSIFICATION: 536

```

```

: ATTORNEY/AGENT INFORMATION:
:
: NAME: Timian, Susan J.
: REGISTRATION NUMBER: 34,103
: REFERENCE NUMBER: 0089,254
: TELECOMMUNICATION INFORMATION:
:
: TELEPHONE: (716) 263-1656
: TELEFAX: (716) 263-1600
: TELE: 978450
:
: INFORMATION FOR SEQ ID NO: 11:
:
: SEQUENCE CHARACTERISTICS:
:
: LENGTH: 610 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
:
: US-08-234-265A-11

```

[illegible]

RESULT 15

RESULT 15  
US-09-182-024A-2  
; Sequence 2, Application US/09182024A  
; Patent No. 6342370  
; GENERAL INFORMATION:  
; APPLICANT: Connolly, Timothy  
; APPLICANT: Rajput, Bhanu

```

1  TITLE OF INVENTION: Homo Slit Polypeptide and Polymers thereof. For pending
2  TITLE OF INVENTION: Same
3  FILE REFERENCE: 640190-271
4  SUB-CLASS: ALIPHATIC POLYMER US 26,7182, 624A
5  CURRENT FILING DATE: 1998-10-29
6  PRIOR APPLICATION NUMBER: 60/063,046
7  PRIOR FILING DATE: 1997-10-31
8  PRIOR APPLICATION NUMBER: 60/096,420
9  PRIOR FILING DATE: 1998-08-13
10 NUMBER OF SEQ ID NOS: 5
11 SOFTWARE: PatentIn Ver. 2.1
12 SEQ ID NO. 2
13 LENGTH: 1523
14 TYPE: PRT
15 ORGANISM: Homo sapiens
16 US-09-183-024A-2

```

```

Q 297 MATCH.      W 29,  Score 278,  Pp 4,  Length 1023;
Best Local Similarity 25.7%,  Pp31. No. 2,553 19;
Matches 94;  Conservative 39;  Mismatches 115;  Indels 118;  Gaps 15;

QY      24  QPSQSSQGVHCFAPKGIHVHVPVPIVGLVYVENGITMLLASSEALPGQLLDL  83
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      725  CPEQCTQME--TVVRCSSNKGRLALPRGPKQVTELYLEGNHUTAV----- 767

QY      84  SQNTASTRIPIIILDI SHNSTIAI PPGIITDANVAI FLAQLGLQGLDEGLFSRLNL 143
      ||||| ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      768  -PRELSAUR--HLTIIDLSNNS-----ISMLTNVIFSNKSHL 801

QY      144  HLDVSNQQLPVP  PVYFPIPGITPLIACNTPTAIPIPIVACIAI QELVYVHLSIQ 202
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      902  STILISNPLPCIDVHAFNGILPSIPVITICGN-----DSSVPRCSNDLITLS-- 850

QY      203  ALPGILSELFPFLIAAARNFCVPLKWFQVWFSHVHTLASDPTPCHPFPVNAQCP 262
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      851  -----HLAIGINPLEDCSLRWLSRWVQAGY--KEPGIARCSSPEPMADR 893

QY      263  ILEIDVAREGPDATTATVITTPVVFVEHTALSSIAPTWLSPTALVATAPPP  ST 320
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      894  LLL-----STTHRECKGQVDINL-- VAFQNACLSSPPQVNN 929

QY      321  APPTVGVPV-----QPDQ--DPSTGL-----NGGCHLGLSTRHH--LACLCPGEF 361
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      929  GTCTQDVEVLYPCALPYSAKNEPVPVINGIQNPAQDGGTCHISDSHNDGFSQCPGEF 988

QY      362  TGLYCE 367
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      989  EGORCE 994
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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Search completed September 17, 2002, 09:51:41  
 Job time: 1518 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compaq Inc.

OM protein - protein search, using sw model

Run on: September 17, 2002, 09:46:24 ; Search time 21 seconds  
(without alignments)  
2736,258 Million cell updates/sec

Title: US-09-944-396-69  
Perfect score: 3135  
Sequence: 1 MCSHVPLLLPLLLLLALGPC.....PLMCFPCGLQSPLEKPKYI 598

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 95089334 residues  
Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_71: \*  
1: pir1: \*  
2: pir2: \*  
3: pir3: \*  
4: pir4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	322	10.3	605	2 J65239	insulin-like growth
2	322	9.6	605	2 A41915	insulin-like growth
3	282	9.0	626	1 RPH01A	platelet glycoprotein
4	281.5	9.0	603	2 J61282	insulin-like growth
5	279.5	9.0	603	2 G61138	insulin-like growth
6	278	8.9	1531	2 T42218	slit 1 protein hom
7	264.5	8.4	420	2 A53531	con-dictal trophob
8	261	8.3	1523	2 T13953	MK3F5 protein - ra
9	255.5	8.1	1469	2 R46665	slit protein 2 pre
10	255.5	8.1	1480	2 A66655	slit protein 1 pre
11	243.5	7.9	312	1 NRP0A2	leucine-rich alpha
12	240	7.7	560	2 A63164	platelet membrane
13	237	7.6	707	2 G77763	neuronal leucine-r
14	231	7.4	1025	2 T42626	secreted leucine-r
15	222.5	7.1	536	2 A43901	leucine autobox-pep
16	214.5	6.9	1545	2 R46224	peroxidase - fru
17	212.5	6.9	361	2 A3860	glutathione S-tran
18	210.5	6.7	4392	2 A38971	polycystic kidney
19	209	6.7	1091	2 A58532	glial cell membran
20	208.5	6.7	392	2 T39068	proline-arginine
21	200	6.4	653	2 T35194	hypothetical prote
22	199	6.2	1328	2 T32007	hypothetical prote
23	194.5	6.2	789	2 T28714	hypothetical prote
24	194.5	6.2	1355	2 T28715	hypothetical prote
25	193.5	6.2	421	2 T46262	hypothetical prote
26	193.5	6.2	721	2 G70760	hypothetical prote
27	192.5	6.1	575	2 T39975	hypothetical prote
28	189	6.0	369	2 G30811	proteoglycan 1 m
29	189	6.0	469	2 S32793	biglycan precursor

30 189 6.0 839 2 T04859  
31 188.5 6.0 440 2 A47540  
32 186 5.9 440 2 A39613  
33 184 5.9 368 1 BGI0N  
34 183 5.8 662 2 S42799  
35 182 5.8 369 2 S42559  
36 181.5 5.8 357 2 S24317  
37 177.5 5.7 2193 2 A55481  
38 176.5 5.6 1495 2 T31434  
39 175 5.6 343 2 A41748  
40 173 5.5 925 2 J62033  
41 172.5 5.5 359 1 NHH0C8  
42 172 5.5 1134 2 T04587  
43 170.5 5.4 2145 2 J64747  
44 170 5.4 907 2 J60176  
45 169.5 5.4 760 2 T06291

ALIGNMENTS

RESULT 1

J65239

insulin-like growth factor acid-labile chain - baboon

C:Species: Papio sp. (baboon)

C:Date: 17-Apr-1997 #sequence\_revision: 99 May 1997 #text\_change: 09 May-1997

C:Accession: J65239

R:Author: P.J. Baxter, R.C.

Biochem. Biophys. Res. Commun. 227, 897-902, 1996

A:Title: The cloning and expression of the baboon acid labile subunit of the insulin-

A:Reference number: J65239; M010:97040714

A:Contents: liver

A:Accession: J65239

A:Molecule type: mRNA

A:Residues: 1-605 -DEL-

C:Comment: This factor is structurally related to prolactin and have insulin-like m

Query Match 10.48; Score 322; DB 2; Length 605;

Best local similarity 46.28; Pred. No. 196-111;

Matches 100; Conservative 39; Mismatches 97; Indels 40; Gaps 11;

QY 7 LILPLILL--LALG-----PGVGG-----QPSGQCSPQ--- -IYVETARQSTT 45

DB 8 LALALLLKKVALGERSLLMALEFTHGAGHAGATACGAYLVHVLSSVNSRMLR 67

QY 46 VPEVTPVTVTVYVPEVTHMFASSPCLPTQTHHSDKLANEPELLL----- 98

DB 9 LPL 126

QY 99 LLSLRKELAFPESTHFAVFAIRLAKG---TGLTERTFSEIRKNTDVSERMLER 155

DB 127 ELLENKESSTAVPT-AYTVALALGLQSSEIETAFPEGLCHLWNT-WSLAV 184

QY 156 VPEVPE 214

DB 185 LITWAPPECELELFEIVLARE SLAVIQALITSGIAPPEPEPEPEPEPEPEPEPE 243

QY 215 LRLAAKRTTCYCLLSWFG---FWVESIVTVA 246

DB 244 LKQRTTETLAAVACATGELAELEWELGSSREVA 279

RESULT 2

A41915

insulin-like growth factor binding complex acid-labile chain precursor - human

R:Alternate names: A-13 labile subunit (ALS)

C:Species: Homo sapiens (man)

C:Date: 31-Dec-1993 #sequence\_revision: 31-Dec-1993 #text\_change: 05 Nov-1999

C:Accession: A41915

R:Author: S.F. Barker, S. Ozols, Camarero, T.J. Davy, J.J. Wood, W.L.

A:Title: Structure and functional expression of the acid labile subunit of the insulin-

A:Reference number: A41915; MIM:92357025

A:Accession: A41915

A>Status: preliminary

A:Molecule type: mRNA; protein

A:Residues: 1-605 <LE0>

A:Cross-references: GR:WR626; RND-j184807; PDB:AAA36947.1; PDB-q184808

A:Experimental source: liver

A:Note: sequence extracted from NCHI backbone (NCBIP:110171)

C:Superfamily: leucine-rich alpha-2-glycoprotein repeat homology

F:75-98/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LE1>

F:99-123/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LE2>

F:124-146/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LE3>

F:147-170/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LE4>

F:171-194/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LE5>

F:195-218/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LE6>

F:219-242/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LE7>

F:243-266/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LE8>

F:267-290/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LE9>

F:291-314/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LE10>

F:315-338/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LE11>

F:339-362/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LE12>

F:363-386/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LE13>

F:387-410/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LE14>

F:411-434/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LE15>

F:435-458/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LE16>

F:459-482/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LE17>

F:483-506/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LE18>

F:507-529/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LE19>

Query Match 9.6%; Score 302; DB 2; Length 605;

Best local Similarity 35.5%; Pred. No. 2,7e-10;

Matches 98; Conservative 40; Mismatches 98; Indels 40; Gaps 11;

QY 7 LLLPLLLL-LALG-----RCVQ-----CPSCQCSQPQ-----TVECTARQGIT 45

DB 8 LALALLLLSWALGPRSLGEGADCTGCAEAG3PACAPACVCSYDIDADELSVFCSSNNIT 67

QY 46 VPROVPTVTVYFFNEITIMIDASSFACILGLQLLDLSDIASIPIPRILL----- 98

DB 68 LDKVVGSTQMLWIDCNLSVVPAAFAFNLSSIGFNIQGRAGISLE-PEALIGFNLCH 126

QY 99 LDISNSLLALDPGLIDANVPAFLRAGL-----LCQIDRLGSRIPNIHDLVSNQLEP 155

DB 127 LHLERNKLSRLATP-AHTPALASLGSNNRLSLETLGLEGLCSWELNLSWNSLAV 184

QY 156 VVFWVQLLQVPLFLACHTFQAQLEFIDACIALMLGTFVYSNLSLALFQLSLSLTF 214

DB 185 LPDAAFKGLGSGRPFIVLARN-PAVYGPALFSGIAFIRPFIQSPNALPAIFANVFWQHP 242

QY 215 FFLAAAFNIPFVYFESWPSFWVFESHVTLA 246

DB 244 LQVIVIDPNI LAAVAPAFGLFALPRLDLSNPVA 276

RESULT 4

NR001A

platelet glycoprotein Ib alpha chain precursor - human

N:Alternate names: membrane glycoprotein Ib alpha chain

N:Ontology: glyocalicin

C:Species: Homo sapiens (man)

C:Date: 28-Dec-1987; sequence revision 28-Dec-1987; rev 2; change 22-Jun-1999

C:Accession: A94174; A60435; A94173; S16945; I55355; A27075; A27102

R:Leiper, J.A.; Chond, D.W.; Fujikawa, K.; Hager, P.S.; Papayannopoulos, T.; Poth, G.I.

Proc. Natl. Acad. Sci. U.S.A. 84, 5615-5619, 1987

A:Title: Cloning of the alpha chain of human platelet glycoprotein Ib: a transmembrane p

A:Reference number: A94174; MIM:87289655

A:Accession: A94174

A:Molecule type: mRNA

A:Residues: 1-626 <LE0>

A:Cross-references: GR:202940; NID:q183499; PDB:AAA52545.1; PDB-q306793

R:Wick, A.N.; Walz, A.; Gerlach-Huber, S.N.; Wenger, P.H.; von Ruger, P.; von Ruger, K.

Thromb. Haemost. 61, 448-453, 1989

A:Title: Isolation and characterization of human blood platelet mRNA and construction

d cloning of a GPIb coding cDNA insert.

A:Reference number: A60435; MIM:90920160

A:Accession: A60435

A:Molecule type: mRNA

A:Residues: 257-467 <WIC>

R:Titani, K.; Takio, K.; Handa, M.; Kuwajiri, Z.M.

Proc. Natl. Acad. Sci. U.S.A. 84, 5610-5614, 1987

A:Title: Amino acid sequence of the von Willebrand factor binding domain of platelet

A:Reference number: A94173; MIM:87489654

A:Accession: A94173

A:Molecule type: protein

A:Residues: 17-315 <TIF>

R:Hess, G.; Schaller, C.; Fritsch, E.F.; von Ruger, P.

Eur. J. Biochem. 199, 389-393, 1991

A:Title: Identification of the His-Asp-His triad in human platelet glypocalicin.

A:Reference number: S16945; MIM:91301149

A:Accession: S16945

A>Status: preliminary

A:Molecule type: protein

A:Residues: 254-277, 282-275, 275-277, 282-283

R:Leiper, J.A.; Leckie, E.H.; McCarthy, B.J.

J. Biol. Chem. 267, 15055-15061, 1992

A:Title: Polymorphism of human glycoprotein Ib alpha results from a variable number o

A:Accession: I55355

A>Status: preliminary; translated from GB,EMBL,DBJ

A:Molecule type: DNA

A:Residues: 412-427 <RES>

A:Cross-references: GB:S34335; NID:3259376; PDB:AA0221.1; PDB-q4249177

A:Note: variant D

C:Comment: Glycoprotein Ib (GPIb), a surface membrane protein of platelets, participa

C:Comment: Platelet activation apparently involves disruption of the macromolecular c

C:Comment: Binding sites for von Willebrand factor and thrombin (the latter site with

C:Comment: Glypocalicin, which is approximately coextensive with the extracellular pa

C:Genetics:

A:Gene: GDB:GPIBA; GPIB

A:Cross-references: GDB:118809; MIM:241200

A:Map position: 17pter-17p12

C:Complex: heterodimer with platelet glycoprotein Ib beta chain (NR001B)

C:Superfamily: platelet glycoprotein Ib alpha chain; leucine rich alpha 2 glycoprotein

C:Keywords: blood coagulation; duplication; glycoprotein; platelet membrane; tandem r

F:1-16/Domain: signal sequence #status predicted -SIG>

F:17-626/Product: platelet glycoprotein Ib alpha chain #status predicted -MPT>

F:48-71/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LE1>

F:72-93/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LE2>

F:94-116/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LE3>

F:117-140/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LE4>

F:141-164/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LE5>

F:165-189/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LE6>

F:189-212/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LE7>

F:213-236/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LE8>

F:237-260/Domain: proline/threonine-rich 9 residue repeats

F:502-540/Domain: transmembrane #status predicted -TRM>

F:541-626/Domain: intracellular #status predicted -INT>

F:37-175/Binding site: carbohydrate (Asn) (covalent) #status experimental

F:308/Binding site: carbohydrate (Thr) (covalent) #status experimental

Query Match 9.0%; Score 282; DB 1; Length 626;

Best local Similarity 24.8%; Pred. No. 4.1e-09;

Matches 169; Conservative 72; Mismatches 244; Indels 190; Gaps 26;

QY 9 FLLTLLTALPTQVQVCTGQVSGVCT -MPTAGACTTGGVGGVGVVGVV - 62

DB 1 MPLLILLLLPSLPHPPICVSKVASHLEVNTKENTLALPDLPRKTLILHSENLLY 60

QY 63 -----GITMLDASSF-----AGLPGIQLLDSNQIASL-----RLPRLLL 98

DB 61 TFSIATIMPTVITQLNLPQCFITLQVCTTFLVCTITLISINQISTQITLQTLFALT 120

QY 59 LQSHSLALFNFI-PTANVPAFLAGLIGLQGLDGLGSPFNHOLDVNSNLEKVP 157

DB 121 LKAGSRRLSLDGLALPCHFLQHLVLYKGRHPTHTFPGILTPTTPKPKLESLANRHTPLP 180  
 QY 129 FVVEHREHTEFLAAGTFLAAGTFLAAGTFLAAGTFLAAGTFLAAGTFLAAGTFLAAGT 174  
 DB 181 AGLLNGLNLDLLQEN-----SLATTPKQFCGSHLHP 215  
 QY 215 LRLAARHPNCTVTLAWTWVRF-----IVTLASPTTFC 253  
 DB 216 APLHSG---NPNLNGCHLLYFPFWQDNAPVYVWFKVGVKAMQSWAGVCCGRSRKPVV 272  
 QY 254 -HPTFNAGELLE- LKVAHPCGFATTTATVPTTFVRF 296  
 DB 273 VYVPCGKFTCLGPHVLYVYVFPFPGVGVATFVVLTKRAHGLWGLYNSGA 322  
 QY 296 LSSSLAPLWLSVALE-----APSPSTAPPTVGPV---PQ 340  
 DB 333 SLDSQMPSSLHTQSTKFTQTPPPRWPNPLHMPSTKFTKSTKFTQTPPPSPPTSPV 362  
 QY 331 PQDQFSTCLNCTTHCTRHHLACLPFFGFTYVKSQWQGTFFSTPTVTPPPPSLT 390  
 DB 393 PPANMMITETP-----SPTTP-----PTSPAPSTPTPTPTPTPT 431  
 QY 391 LGPP---VSPISLVGLQPLQSS--VQPSPTPTPNLSSPKPVLPLP--LPASLA 443  
 DB 432 IATSTILVSATSLTKSTLTITKPVSLLESTKTKTPELDQVFKLVGLQHLSSRN 491  
 QY 444 EYVYQLPNAIYSVWVME-----ICPV PEGHACGEAHT 480  
 DB 492 P--PPIHPD---PCTLPPTGPVVLGHPWLPASVVIITLSWGHVFPQATDSGGCAI 545  
 QY 481 PPVHSHNAPVTQAREGNP---IT---APALAAVLLAALAAVAAVYVRRGRAMAAA 533  
 DB 546 ITATQTHIFIQPGQGVIVPAWILFTPGSLPTPESSILFWVPDNCVGVPLVACPRPSAL 605  
 QY 534 AQGRQV 539  
 DB 606 SQGRQV 611

## RESULT 4

JC1282

Insulin-like growth factor binding protein acid labile chain precursor rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 30-Sep-1993 #sequence\_revision 69-Sep-1993 #text\_change 21-Jul-2000

C:Accession: JC1282

R:Pal J. Baxter, R.C.

Biochem. Biophys. Res. Commun. 188, 304-309, 1992

R:Title: Molecular cloning of the acid labile subunit of the rat insulin like growth factor

R:Reference number: JC1282; MUID:93038676

A:Accession: 551262

A:Molecule type: mRNA

A:Residues: 1-603<NAK>

A:Cross-references: 2R-546785; MID:92589002; FIDR:AA024770.2; FID:q579534

A:Experimental source: liver

A>Note: the authors translated the codon AAG for residue 63 as Arg, AAA for residue 205

C:Superfamily: leucine rich alpha 2 glycoprotein repeat homology

F1-27/29:main signal sequence status predicted <SIG>

F1-28-603/Product: insulin like growth factor binding protein, acid labile chain #status

F1-267-290/Domain: leucine-rich alpha-2 glycoprotein repeat homology <LRR>

## Query Match

Best local similarity 9.0%; Score 281.5; DB 2; Length 603;

Matches 90; Conservative 49; Mismatches 166; Indels 37; Gaps 11;

QY 6 PLELLILL-LALGP-GVQG-----CPSCGQV-SQPG-----TVFCTARQGT 45  
 DB 8 PALVLLAFWALGPGYLOGTIDPGASALAEQPGCPVCTCSYDIYHIDLSVPSRRNLQ 67  
 QY 46 VPRVPEPTVHYVYVNTIMLDASSTVAGPSIQLHNSQGLASRLREPLLI----- 98  
 DB 68 IPHETPVSDFALWFPNNSIPSAFENISLIDELNIGESWIPSTF-PGALITGLNLYH 126  
 QY 99 ILSHNCGLALIDVTHLPTANVVALKACLGQGLQGLPGLPGLPGLPGLPGLPGLPGLP 157  
 DB 127 TTEETLQAAVTFHTKATVQVQPIIDELHLLHGLHGLHGLHGLHGLHGLHGLHGLH 186  
 QY 176 TVIEHLETFELFAGTFLAQDPEFLTAATAATHTTVHKLALAEKGLPPTTP 216  
 DB 187 DIVFQGLCHHHLVAGN-KLIVL-FALDGLGEPFLGLASERNALESVPANVTHHGGQ 245  
 QY 217 LLAARHTPTVPLSWTC- IWRHSHVTLA 246  
 DB 246 KYEDENLITAVAPFLQFLQWALWGLHLSHNEVA 274

## RESULT 6

T42218

slit-1 protein homolog - rat

R:Alternate names: MGF4 protein

C:Species: Rattus norvegicus (Norway rat)

C>Date: 03-Nov-1993 #sequence\_revision 03-Dec-1999 #text\_change 21-Jul-2000

C:Accession: T42218

R:Biological X: Nishijima, E., Kojima, T., Nemura, N., Seki, H., Ohara, O.

Genomics 51, 27-34, 1998

A:Title: Identification of high-molecular-weight proteins with multiple EGF-like motif

A:Reference number: T42218; MUID:98360089

A:Accession: T42218

A:Status: preliminary; translated from GR/EMBL/DBEM

A:Molecule type: mRNA

A:Residues: 1-1531<NAK>

QY 170 HLSRSLAIPGCTTPTAVWPAFLACVCLQVSDPQVPSLPSLPSLPSLPSLPSLPSLPS 157  
 DB 174 HIFPPEHFAVCTPTTPSCASISGNTIDEDSLPDLQHLWGLASGLAVLQ 187  
 QY 176 IVYRGLRGLTRKLAGTTRIAQRLHGLAALQHLHNSNLSQALPGLHSLPTEFL 217  
 DB 189 TVGQVTHLIVVACHFTTTLGALPGLTTFELSSSRLKFAVAVTVHDELK 246  
 QY 218 LAAARHPNCTVPLSWTC IWRHSHVTLA-PEDETHPP 256  
 DB 247 LYLERNLITAVAPGLQFLQWALWGLHLSHNEVA 274

## RESULT 5

JC6128

insulin-like growth factor binding complex acid labile chain - mouse

C:Species: Mus musculus (house mouse)

C>Date: 23-Mar-1997 #sequence\_revision 09-May-1997 #text\_change 05-Nov-1999

C:Accession: JC6128

R:Boisclair, Y.R., Soto, D., Hsieh, S., Hurst, K.R., 001, G.T.

Proc. Natl. Acad. Sci. U.S.A. 93, 10028-10033, 1996

A:Title: Organization and chromosomal localization of the gene encoding the mouse aci

A:Reference number: JC6128; MUID:96414591

A:Accession: JC6128

A:Molecule type: DNA

A:Residues: 1-603<NAK>

A:Cross-references: 09-06999; MID:412412; FIDR:AA012270.1; FID:q1621613

C:Comment: This protein is a serum protein and it is of the tetraary complex in the ph

C:Genetics: als

A:Gene: als

A:Map position: 17

## Query Match

Best local similarity 8.9%; Score 278.5; DB 2; Length 603;

Matches 90; Conservative 48; Mismatches 101; Indels 35; Gaps 10;

QY 6 PLELLILL-LALGP-GVQG-----CPSCGQV-SQPG-----TVFCTARQGT 45  
 DB 8 PALVLLAFWALGPGYLOGTIDPGASALAEQPGCPVCTCSYDIYHIDLSVPSRRNLQ 67  
 QY 46 VPRVPEPTVHYVYVNTIMLDASSTVAGPSIQLHNSQGLASRLREPLLI----- 98  
 DB 68 IPHETPVSDFALWFPNNSIPSAFENISLIDELNIGESWIPSTF-PGALITGLNLYH 126  
 QY 99 ILSHNCGLALIDVTHLPTANVVALKACLGQGLQGLPGLPGLPGLPGLPGLPGLPGLP 157  
 DB 127 TTEETLQAAVTFHTKATVQVQPIIDELHLLHGLHGLHGLHGLHGLHGLHGLHGLH 186  
 QY 176 TVIEHLETFELFAGTFLAQDPEFLTAATAATHTTVHKLALAEKGLPPTTP 216  
 DB 187 DIVFQGLCHHHLVAGN-KLIVL-FALDGLGEPFLGLASERNALESVPANVTHHGGQ 245  
 QY 217 LLAARHTPTVPLSWTC- IWRHSHVTLA 246  
 DB 246 KYEDENLITAVAPFLQFLQWALWGLHLSHNEVA 274

Query Match	8.42	Score	264.5	DB 2	Length	420	
Best Local Similarity	28.10	Pred. NC	2.7e-08				
Matches	103	Conservative	44	Mismatches	121	Models	99
							Gaps

[illegible]





F:791-813/Domain: Leucine-rich alpha-2-glycoprotein repeat homolog - LF87  
 F:815-838/Domain: Leucine-rich alpha-2-glycoprotein repeat homolog - LF88  
 F:846-868/Domain: Leucine-rich alpha-2-glycoprotein repeat homolog - LF89  
 F:1028-1041/Domain: EGF homolog - LF90  
 F:1068-1099/Domain: EGF homolog - LF91  
 F:1115-1148/Domain: EGF homolog - LF92

Query Match: 9.1%; Score 255.5; DB: 2; Length 1490.  
 Best Local Similarity: 21.4%; Pred. No. 3.8e-07;  
 Matches 105; Conservative 52; Mismatches 168; Indels 165; Gaps 14;

QY 24 CPSCGCGSOTVETCTARCTVPRVP .....PDTGVL 58  
 DB 519 CPAMCHC-EGTVVDCVGRPIKPIPRDIPHTTEILLNNELGRISDDGLFGRPLRYKLE 577  
 QY 59 VPNGITMI DASSPACIPGQITLISQNTAS-----LPLPPLLLDLSHNSLALFPG 112  
 DB 578 LKNQLTGTRPNAPFACASHIQELQENKIKPIISKMPILGIHQIKLNLYNQSLQVMPG 637  
 113 ILDTAN-----VEALPLAGIGIGQLDPSGLFSLPLNLHLDV--- 148  
 DB 638 SFEHLNLSLNLASPNFNCHLAWFAECVKKSLNSRAACGAPSKVRQVQTKDPLHS 697  
 QY 149 -----SDNLERVP--PV----- 159  
 DB 698 EFKCSNSESGTGVGPPSPITGIVVACSPNLKELPGIPAIETSELYLESNEIROI 757  
 QY 160 -----IRTRILTLRLANTRIAQLPPHLAGIALQELDS-----NL 199  
 DB 758 HYKIRHLRLSLTGLDS--NQITILSNYTFANLTKLSTLISYNKLCLOLRHALSGNL 816  
 QY 206 SLQALPTDLSGTPR-----LELLAAAEFENCVCPLSGWGNWFSHWTLASFEET 251  
 DB 817 RVVSLHGNRISMLPGSFEEDLSLTHIALGNSPLYDGLKWFSDWKLDV---EPGLA 873  
 QY 252 KCHPKNAGRLLELDYADFGCPATTTTATVPTTPPVVREPTALSSSLAPTWSPTAPA 311  
 DB 874 KCAPEGMKTKLLSLSPSSEFCGKVRNLLAKGNACFEQGNQACV-----ALPQ 927  
 QY 312 TEAFSTFSTAFPTVGVPGI-----GQEPSTLPGSTVHDTGKHILA-LPFG 960  
 DB 928 PFGV-----EQGPTGHEKHPEPMILQVYGNICPNNAITVLEFGWFSQVAPG 975  
 QY 361 FTGLYCESOM 370  
 DB 977 YTGACETNI 986

Result 11  
 NB0042  
 C:Species: Homo sapiens (man)  
 C:Date: 27 Nov 1985 #sequence\_revision 27-Nov-1985 #text\_change 05-Nov-1998  
 R:Tababashi, N.; Takabashi, Y.; Katam, P.W.  
 Proc. Natl. Acad. Sci. U.S.A. 82: 1966-1970, 1985  
 A:Title: Periodicity of leucine and tandem repeat structure of a 24 amino acid segment in the  
 A:Reference number: A03211; MUID:86166241  
 A:Accession: A03211  
 A:Molecule type: protein  
 A:Postions: 1-31; 27-28

C:Comment: The function of this plasma protein is not known.  
 C:Suprafamily: Leucine-rich alpha-2-glycoprotein; leucine rich  
 C:Keywords: duplication; glycoprotein; plasma; tandem repeat  
 F:58-81/Domain: Leucine-rich alpha-2-glycoprotein repeat homolog - LF93  
 F:82-105/Domain: Leucine-rich alpha-2-glycoprotein repeat homolog - LF94  
 F:106-129/Domain: Leucine-rich alpha-2-glycoprotein repeat homolog - LF95  
 F:130-153/Domain: Leucine-rich alpha-2-glycoprotein repeat homolog - LF96  
 F:154-177/Domain: Leucine-rich alpha-2-glycoprotein repeat homolog - LF97  
 F:178-201/Domain: Leucine-rich alpha-2-glycoprotein repeat homolog - LF98  
 F:202-225/Domain: Leucine-rich alpha-2-glycoprotein repeat homolog - LF99  
 F:226-249/Domain: Leucine-rich alpha-2-glycoprotein repeat homolog - LF100

F:262-289/Domain: Proteoglycan coreglycosyl terminal homology - LF101  
 F:290-313/Domain: Proteoglycan coreglycosyl terminal homology - LF102  
 F:314-337/Domain: Proteoglycan coreglycosyl terminal homology - LF103  
 F:338-361/Domain: Proteoglycan coreglycosyl terminal homology - LF104  
 F:362-385/Domain: Proteoglycan coreglycosyl terminal homology - LF105  
 F:386-409/Domain: Proteoglycan coreglycosyl terminal homology - LF106  
 F:410-433/Domain: Proteoglycan coreglycosyl terminal homology - LF107  
 F:434-457/Domain: Proteoglycan coreglycosyl terminal homology - LF108  
 F:458-481/Domain: Proteoglycan coreglycosyl terminal homology - LF109  
 F:482-505/Domain: Proteoglycan coreglycosyl terminal homology - LF110  
 F:506-529/Domain: Proteoglycan coreglycosyl terminal homology - LF111  
 F:530-553/Domain: Proteoglycan coreglycosyl terminal homology - LF112  
 F:554-577/Domain: Proteoglycan coreglycosyl terminal homology - LF113  
 F:578-601/Domain: Proteoglycan coreglycosyl terminal homology - LF114  
 F:602-625/Domain: Proteoglycan coreglycosyl terminal homology - LF115  
 F:626-649/Domain: Proteoglycan coreglycosyl terminal homology - LF116  
 F:650-673/Domain: Proteoglycan coreglycosyl terminal homology - LF117  
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 C:Genetics:  
 A:Gene: SL12

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 Best Local Similarity 21.6%; Pos 4; <6>64  
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 QY 24 CPSQSQSQPQVETARQGTTPRQVPPQVGVYVFENGITMLDASSFAGLPGQLQLDL 83  
 DB 223 CPSEKPLD-XXVSCNKGLKVLPGIKPKDVTGLYDNGQPTLV-FKLSNVKRLTLDL 280  
 QY 84 SQNGIASL-----LPRLLLDLSHNSLIALRPGILDTANVFALRAGLGLQQLDSELF 137  
 DB 281 SNKRISLNSQXFSNNTOILLILSYNRLRCIPPRTFD-----GLKSL----- 323  
 QY 138 SRLKRLHDLVSNQLEPVPVIRGLGLTRKRLAGNTRKLAGLREEDLAGLAALQELDVS 197  
 DB 424 -RLLSLGNDS-----VVP----- 337

QY 198 NLSLQALPGSLGSLPRKRLIAAANPNCVPLSWGPPWVRESIVILASPEETRCHEPP 257  
 DB 338 ---EGAFNLSA---LSHLAGANPVGTCNMGWISDWVKSFY--KPEGLAKACAPG 366  
 QY 258 KNAGRLLELDVAFVCPATTITTAIVTPTRVVRPEALSSSLAPTTLWLTAPATEAPSP 317  
 DB 387 EMARILLITTPSKKFTQ-----GPMDDITIOAKNCPCLSN 421  
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## RESULT 15

A34901

lysine carboxypeptidase (87.4.4.17.3) 83K chain - human

C:Species: Homo sapiens (man)

C:Date: 20-Jul-1990 #sequence\_revision 20 Jul 1990 #text\_change 05-Nov-1999

C:Accession: A34901

R:Tan, F.; Weerasinghe, D K.; Skidgel, P A.; Tamai, H.; Kaul, P K.; Robinson, I.B.; Schi

J. Biol. Chem. 265, 13-19, 1990

A:Title: The deduced protein sequence of the human carboxypeptidase N high molecular wei

Reference number: A34901; MUID:90094386

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-536 &lt;TAN&gt;

A:Cross-references: GR-105158; NID:9179935; PID:AAA51921.1; PID:9179936

C:Genetics:

A:Gene: GDB:ACHP

A:Cross-references: GDB:127893

A:Map position: 6q25.3-6q26

C:Superfamily: leucine-rich alpha-2-glycoprotein repeat homology

C:Keywords: hydrolase; metallo carboxypeptidase

F:77-100/Domain: leucine rich alpha-2 glycoprotein repeat homology &lt;LRR1&gt;

F:101-124/Domain: leucine rich alpha-2 glycoprotein repeat homology &lt;LRR2&gt;

F:125-148/Domain: leucine rich alpha-2 glycoprotein repeat homology &lt;LRR3&gt;

F:149-172/Domain: leucine rich alpha-2 glycoprotein repeat homology &lt;LRR4&gt;

F:173-196/Domain: leucine-rich alpha-2-glycoprotein repeat homology &lt;LRR5&gt;

F:197-220/Domain: leucine rich alpha-2-glycoprotein repeat homology &lt;LRR6&gt;

F:221-244/Domain: leucine rich alpha-2-glycoprotein repeat homology &lt;LRR7&gt;

F:245-268/Domain: leucine rich alpha-2-glycoprotein repeat homology &lt;LRR8&gt;

F:269-292/Domain: leucine-rich alpha-2-glycoprotein repeat homology &lt;LRR9&gt;

F:293-316/Domain: leucine-rich alpha-2-glycoprotein repeat homology &lt;LRR10&gt;

F:317-340/Domain: leucine-rich alpha-2-glycoprotein repeat homology &lt;LRR11&gt;

F:341-364/Domain: leucine-rich alpha-2-glycoprotein repeat homology &lt;LRR12&gt;

Query Match 7.1%; Score 222.5; DB 2; Length 536;  
 Best Local Similarity 34.8%; Pred. No. 9.8e-06;  
 Matches 70; Conservative 27; Mismatches 47; Indels 17; Gaps 7;  
 QY 25 PSQSQSQPQVETARQGTTPRQVPPQVGVYVFENGITMLDASSFAGLPGQLQLDL 84  
 DB 2 PMQCTGF-VQVFCSDFTLATVILPNTENIIVPTTPTTPTTPTTPTTPTTPTTPTTPTT 60  
 QY 85 QNGIASL-----LPRLLLDLSHNSLIALRPGILDTANVFALRAGL-----LQQLDEG 135  
 DB 61 DTQLCQFRPDADFGLPRLDELEVTGSSTINISINIF--SNISLCKLTINFMLEALPEG 118  
 QY 136 LESPLRLHDLVSNQLEPVP-VVIRGLGLTRKRLAGNTRKLAGLREEDLAGLAALQEL 194  
 DB 119 LFQHLAALESILHQNQLQALPRILFQPIIHKIINAGNI-LAQIPPELPHPTISTQLD 177  
 QY 195 DVSNISLQALPGSLGSPRL 215  
 DB 178 KLSNNALSCLP---QGVFQKL 195

Search completed: September 17, 2002, 09:53:44  
 Job time: 44.6 sec







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FT REPEAT 53 73
FT REPEAT 74 96
FT REPEAT 98 120
FT REPEAT 121 144
FT REPEAT 145 168
FT REPEAT 169 192
FT REPEAT 194 216
FT REPEAT 217 240
FT REPEAT 242 264
FT REPEAT 265 288
FT REPEAT 289 312
FT REPEAT 313 336
FT REPEAT 338 360
FT REPEAT 361 384
FT REPEAT 386 408
FT REPEAT 409 432
FT REPEAT 433 456
FT REPEAT 458 480
FT REPEAT 482 504
FT REPEAT 505 530
FT REPEAT 531 554
FT CARBOHYD N-LINKED (GLUCNA...) (POTENTIAL)
FT CARBOHYD 85 85
FT CARBOHYD 96 96
FT CARBOHYD 368 368
FT CARBOHYD 515 515
FT CARBOHYD 580 580
SQ SEQUENCE 605 AA 66110 MW: 93719946.25823650 CR664;

Query Match 10.3k; Score 322; DB 1; Length 605;
Best local Similarity 36.2k; Pred. No. 1e-11;
Matches 100; Conservative 49; Mismatches 97; Indels 40; Gaps 11;

QY 7 LLLPILLI--LALG-----RWQ-----CPSCGCSQSO -TVCTARQGT 45
DB 8 LALLLLSSWVAIPPSIPGAFPTGPAFGPA'DATCA'SYDVEYNELSVETSSPNT 67
QY 46 VPPIVPIVILYVEFCITMILASSFAGIPGLQILMSQJASIRLPRLL----- 98
DB 68 LPDGLPGTQALWLSNNISIPPAAPENISLAPINQDQLGSIF-PQALLGLENLCH 126
QY 99 LLLSINSITAIPTGTTTANVEAIFRAGI---IQQIDFELSPNLHLVDSDNQLEP 155
DB 127 LHLRRGRLRSVATF--AVTALALIGLSSNNKLSRFRERFRTGSLNMDI NIGWRSIAV 184
QY 156 VP-IVVIRLRLTLRTAGNTRTAGIWDPI AGLAALQELVSNLSLQALPGDLSCLPP 214
DB 185 LPDAARFRLGGLPFLVIAGN-PLAVIQPALFSGIAFLIPPLISPAIPATKANVFAQLPP 243
QY 215 LRLIAAANKPNCVCLPSWFQ IWNISRHVLA 246
DB 244 LKLVIVNPIIAAVAPGAFICIAIPWIPLSHPVA 274

RESULT 2
ALIS_HUMAN STANDARD: PRI: 605 AA.
AC: P35858;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Insulin-like growth factor binding protein complex acid labile chain
DE precursor (ALS).
GN IGFALS OR ALS.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID 9606;
RN [1]
RZ SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE Liver;
RX MFLINP-92457025; PubMed-1376671;

```

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RA Leong S.R., Baxter R.C., Camerato T., Bai J., Wood W.L.;
RT "Structure and functional expression of the acid labile subunit of
RL the insulin-like growth factor-binding protein complex.";
RN Mol. Endocrinol. 6:870-876(1992).
RP SEQUENCE FROM N.A.
RA Frankland J.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 28:35.
RX MEDLINE-8930584; PubMed-2473065;
RA Baxter R.C., Martin J.L., Beniac V.A.;
RT "High molecular weight insulin like growth factor binding protein
complex. Purification and properties of the acid-labile subunit from
human serum.";
RN J. Biol. Chem. 264:11843-11848(1989).
CC 1 FUNCTION: INVOLVED IN PROTEIN-PROTEIN INTERACTIONS THAT RESULT
CC IN PROTEIN COMPLEXES, RECEPTOR-LIGAND BINDING OR CELL ADHESION.
CC 1 SUBUNIT: FORMS A TERNARY COMPLEX OF ABOUT 140 TO 150 kDa WITH
CC IGF-I OR IGF-II AND IGFBP-3.
CC 1 SUBCELLULAR LOCATION: Extracellular.
CC 1 TISSUE SPECIFICITY: PLASMA.
CC 1 SIMILARITY: CONTAINS 20 LEUCINE-RICH REPEATS (LRR).
CC This SwissProt entry is copyright. It is produced through a collaboration
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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/monopoly
CC or send an email to licensed@sib-sib.ch).
DB EMBL: M86826; AAA36047.1;
DB EMBL: A1031724; CAC36078.1;
DB PIR: A41915; A41915.
DB HSSP: P23945; IXON.
DB MIM: 601489;
DB InterPro: IPR001611; LRR.
DB InterPro: IPR000483; LRR_Cterm.
DB InterPro: IPR000372; LRR_Nterm.
DB InterPro: IPR003592; LRR_Cut.
DB InterPro: IPR003591; LRR_Typ.
DB Pfam: PF00560; LRR; 19.
DB Pfam: PF01463; LRRCT; 1.
DB Pfam: PF01462; LRRNT; 1.
DB PRINTS: PR00019; LEURICHRPT.
DB SMART: SM00370; LRR; 2.
DB SMART: SM00082; LRRCT; 1.
DB SMART: SM00013; LRRNT; 1.
DB SMART: SM00369; LRR_Typ; 11.
KW Glycoprotein, Leucine-rich repeat, Repeat, Signal.
FT SIGNAL 1 27
FT CHAIN 28 605
FT REPEAT 53 73
FT REPEAT 74 96
FT REPEAT 98 120
FT REPEAT 121 144
FT REPEAT 145 168
FT REPEAT 170 192
FT REPEAT 193 216
FT REPEAT 217 240
FT REPEAT 242 264
FT REPEAT 265 288
FT REPEAT 289 312
FT REPEAT 313 336
FT REPEAT 338 360
FT REPEAT 361 384
FT REPEAT 386 408
FT REPEAT 409 432
FT REPEAT 433 456
FT REPEAT 458 480
FT REPEAT 482 504

```

"Structure and functional expression of the acid labile subunit of the insulin-like growth factor-binding protein complex.";

Mol. Endocrinol. 6:870-876(1992).

SEQUENCE FROM N.A.

Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.

[3]

SEQUENCE OF 28:35.

MEDLINE-8930584; PubMed-2473065;

Baxter R.C., Martin J.L., Beniac V.A.;

"High molecular weight insulin like growth factor binding protein complex. Purification and properties of the acid-labile subunit from human serum.";

J. Biol. Chem. 264:11843-11848(1989).

FUNCTION: INVOLVED IN PROTEIN-PROTEIN INTERACTIONS THAT RESULT

IN PROTEIN COMPLEXES, RECEPTOR-LIGAND BINDING OR CELL ADHESION.

SUBUNIT: FORMS A TERNARY COMPLEX OF ABOUT 140 TO 150 kDa WITH

IGF-I OR IGF-II AND IGFBP-3.

SUBCELLULAR LOCATION: Extracellular.

TISSUE SPECIFICITY: PLASMA.

SIMILARITY: CONTAINS 20 LEUCINE-RICH REPEATS (LRR).

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EMBL: M86826; AAA36047.1; -

EMBL: A1031724; CAC36078.1; -

PIR: A41915; A41915.

HSSP: P23945; IXON.

MIM: 601489; -

InterPro: IPR001611; LRR.

InterPro: IPR000483; LRR\_Cterm.

InterPro: IPR000372; LRR\_Nterm.

InterPro: IPR003592; LRR\_Cut.

InterPro: IPR003591; LRR\_Typ.

Pfam: PF00560; LRR; 19.

Pfam: PF01463; LRRCT; 1.

Pfam: PF01462; LRRNT; 1.

PRINTS: PR00019; LEURICHRPT.

SMART: SM00370; LRR; 2.

SMART: SM00082; LRRCT; 1.

SMART: SM00013; LRRNT; 1.

SMART: SM00369; LRR\_Typ; 11.

Glycoprotein, Leucine-rich repeat, Repeat, Signal.

SIGNAL 1 27

CHAIN 28 605

REPEAT 53 73

REPEAT 74 96

REPEAT 98 120

REPEAT 121 144

REPEAT 145 168

REPEAT 170 192

REPEAT 193 216

REPEAT 217 240

REPEAT 242 264

REPEAT 265 288

REPEAT 289 312

REPEAT 313 336

REPEAT 338 360

REPEAT 361 384

REPEAT 386 408

REPEAT 409 432

REPEAT 433 456

REPEAT 458 480

REPEAT 482 504



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FT REPEAT 505 530 LRR 20.
FT CARBOHYD 64 64 N-LINKED (GLCNAC) (POTENTIAL)
FT CARBOHYD 85 85 N-LINKED (GLCNAC) (POTENTIAL)
FT CARBOHYD 96 96 N-LINKED (GLCNAC) (POTENTIAL)
FT CARBOHYD 368 368 N-LINKED (GLCNAC) (POTENTIAL)
FT CARBOHYD 515 515 N-LINKED (GLCNAC) (POTENTIAL)
FT CARBOHYD 580 580 N-LINKED (GLCNAC) (POTENTIAL)
SQ SEQUENCE 605 AA: 66034 MW: 66562A23CB918FC CRC64,

Query Match 9.66; Score 402; DP 1; Length 605;
Best Local Similarity 25.5%; Prod No. 1 50 10;
Matches 98; Conservative 40; Mismatches 38; Gaps 11.

Q7 7 LLLPLLLL LALG... PRVQ... CPSSGCGSQ... IVECIAR... 45
DB 8 LALALLLSWALGSPRESLEAGETGTEARAGPACPAACVSYLAEELSVCSSKRLR 67

Q7 16 VPDPVPTVGVLYFTNGITMLDASSEACI PGLIGLIDISQNCASLSEFP... 98
DB 68 LDPGVGGTQALWELGNLSSVPPAFAONLSSGLFNLGGGGLSLF-PQALIGLENLCH 126

Q7 99 LQLSHSLHLEFGILDTANVEALSLAGL... LQQLRRGLFSFENFHLIVSINLIER 155
DB 127 LHLERNQLRSLAGTF--AHTPALASGLSNNRFSPLRDLGFLGSLWDLNCLNSLAV 184

Q7 156 VP-PVIRGLRGLTHPLACNTPIALPPEDLAGLAALGELVSNLSGLATPRLSGIIPP 214
DB 185 LPDAEPGLGSLPELVLAGN-PLAYLQALFSLAFIPDELDRNALPAIKANVEVQLPR 243

Q7 215 LRIIAARNPENCPLSNEG---PWVPESHVTLA 245
DB 244 LQKLYLDNI IAAVARGAELGLKALRWLDLSHNVVA 279

RESULT 3
GAC1 HUMAN
ID GAC1 HUMAN STANDARD; PRT; 713 AA.
AC Q75325;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Glioma amplified on chromosome 1 protein precursor
GN GAC1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homin.
OX NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
RC TISSUE=Glial tumor;
PX MEDLINE=98324709; PubMed 9562332;
RA Maitoy B., Almeida A., Zhu X.X., Vogt N., Tyagi P., Muleris M.,
RA Dutrillaux A.-M., Dutrillaux B., Foss B., Hanash S.;
RT "GAC1, a new member of the leucine-rich repeat superfamily on
RT chromosome band 1q32.1, is amplified and over-expressed in malignant
RT gliomas.";
RL Oncogene 16:3667-3672(1998)
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (potential).
CC -!- TISSUE SPECIFICITY: OVEREXPRESSED IN MALIGNANT GLIOMAS.
CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -!- SIMILARITY: CONTAINS 11 LEUCINE-RICH REPEATS (LRR).
-----
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entities requires a license agreement (see http://www.isb-sib.ch/announc
or send an email to license@isb-sib.ch)).
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EMBL: AF030435; AAC30792 1; -

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DR MM: 605492; -.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR004598; Ig_C2.
DR InterPro: IPR001611; LRR.
DR InterPro: IPR000483; LRR_Cterm.
DR InterPro: IPR000372; LRR_Nterm.
DR InterPro: IPR004592; LRR_Out.
DR InterPro: IPR003591; LRR_type.
DR Pfam: PF00047; Lrr_1.
DR Pfam: PF00560; Lrr_10.
DR Pfam: PF01463; LrrPT_1.
DR Pfam: PF01462; LrrPT_1.
DR Pfam: PF00319; LRRICHPTT.
DR SMART: SM00408; IGG2; 1.
DR SMART: SM00470; LRR; 6.
DR SMART: SM00082; LRRCT; 1.
DR SMART: SM00013; LRRNT; 1.
DR SMART: SM00369; LRR_Type_2.
KW Immunoglobulin domain, Transmembrane, Glycoprotein, Repeat;
FW Leucine-rich repeat; Signal.
FT SIGNAL 1 18 POTENTIAL.
FT CHAIN 19 713 GLIOMA AMPLIFIED ON CHROMOSOME 1 PROTEIN.
FT L-MAIN 19 630 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 631 651 POTENTIAL.
FT DOMAIN 652 713 CYTOPLASMIC (POTENTIAL).
FT REPEAT 92 115 LRR 1.
FT REPEAT 116 139 LRR 2.
FT REPEAT 140 163 LRR 3.
FT REPEAT 165 187 LRR 4.
FT REPEAT 188 211 LRR 5.
FT REPEAT 213 235 LRR 6.
FT REPEAT 236 259 LRR 7.
FT REPEAT 261 283 LRR 8.
FT REPEAT 309 333 LRR 9.
FT REPEAT 334 357 LRR 10.
FT REPEAT 359 385 LRR 11.
FT DOMAIN 438 504 IG-LIKE C2-TYPE DOMAIN.
FT DISULFID 445 497 BY SIMILARITY.
FT CARBOHYD 94 94 N-LINKED (GLCNAC) (POTENTIAL).
FT CARBOHYD 381 381 N-LINKED (GLCNAC) (POTENTIAL).
FT CARBOHYD 555 555 N-LINKED (GLCNAC) (POTENTIAL).
FT CARBOHYD 583 583 N-LINKED (GLCNAC) (POTENTIAL).
SQ SEQUENCE 713 AA: 78798 MW: 60809P344069496 QRC64;

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Query Match 9.66; Score 282.5; DP 1; Length 713;  
 Best Local Similarity 22.5%; Prod No. 2 59;  
 Matches 176; Conservative 66; Mismatches 255; Gaps 27;

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Q7 7 LLLPLLLLALG-----PGVQCGPSGCGQS-----QPTVFCIARQGITV 46
DB 4 LVAPLLAWAGATAAVVFWVFWVPCPPQACQIRPWYTPSSYFEATVDCNLFIAV 63
Q7 47 PRDVP-----PQIVGLV 58
DB 64 PPAIPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAP 123
Q7 59 VEDEITTLKASFAEATFETLTSQRT---ASLFEELLLLSHSLALE-- 110
DB 124 LELNGTETLTREFACTASTQELVYRHNQVYFAFAFASCTENIPIHNSNLFATDSP 183
Q7 111-----PQILD-----FANVLAFLACLOGLQGLSGLRNHLDD 147
DB 184 WFEMLPNIFITMTGNKVKVDATIMNPFELARIPSLVLGNNIPETSPYAFETQSLES 243
Q7 148 VSDNQLRVP-----PVIR----- 161
DB 244 FVPEIAPVAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAP 303
Q7 162-----GLSGLFELPGLA-NIPFAQLPPELGLA-NAAQLGLVFNLSFGLDGLFTPEL 217
DB 304 FALVNIPELTKDTNNPRLSFTHPAFPHHLPQMETLMIINNALSALHGTTFVSPDNIQF 363

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QY 218 TAAAPNPNCVCLSWFGPWPVESHVTLASPEETPCHEFPKKNAGRLLELLDYADFGCPAT 277  
 BB 364 VGLRNPTECLCVIPWNP--AARGVVFIRPQSTLTAEPPHLLGLVPPVPPFPM-----416  
 QY 278 TTTATVPTTRPVREPTALSSSLAPTWLSPATFATEAPSPSTAPPTVGPVQPODCPPS 337  
 DB 417 -FDHCLPLISPSRFPPLSQVSGESMVLGCRALRAEPPEIYVWVTPAGLRETP-----467  
 QY 338 TGLNGTCHLCTPHILAC-LPPKPF-----TGLY-CPSQ-----369  
 BB 468 -----AHACRR-----CVTPPEETFLPVTAKEAGLYTCVALNGLVGLAKTVSVVWVKR 516  
 QY 370 -----MGQCTRESPPVPP-----PPPSLTIGTEPVSPTSLRVLGSLPYLGSSS 413  
 DB 517 ALLQGRGQGLRLRVQTFHYHIIILSWVTPFNTVSTNLTWSASLEG QGAT 570  
 QY 414 VQLPSRLTYPMI SQPKPIVTLPI PASIAPVYVTVQLPPNATYSVVMPIGPGVPPFRR 473  
 DB 571 -----ALARLPGRGTHSYNITRLLQATYEWACL-----GV 599  
 QY 474 AGGEAHTPPA --VHSNEAPVTOAPEGNLPLILIA-PALAAVILAA-LAAVGAAYCVPPG- 527  
 DB 600 AFADAHTOLACVWARTKATSCHEALGRPGLTALIALAVILLIAGLAHLGTGQPPKGV 659  
 QY 528 ---PAMAAAGCFKCVTGS-----ATTELETVKVFLEIPIKATISGDA:PSNSPFEVIL 588  
 DB 660 GGRPPIPPMAAFWGSAPSVPVVSAPVLT-----PWNPKPK-----IPRSSEGETIL 706

RESULT 4  
 GPHA\_HUMAN STANDARD: PRT: 626 AA.  
 AC P07359;  
 DT 01-APR-1988 (Rel. 07, Created)  
 DT 01-APR-1988 (Rel. 07, Last sequence update)  
 DT 01-MAR-2002 (rel. 41, last annotation update)  
 DE Platelet glycoprotein Ib alpha chain precursor (GP-IR alpha) (GP1BA)  
 DE (CD42B-alpha) (CD42b) [Contains: Glycocalicin].  
 GN GP1BA.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE  
 RX MEDLINE=87289655; PubMed=400400.  
 RA Lopez T A., Cheng S W., Fujikawa K., Nagasawa F., Nagasawa F., Nagasawa F.,  
 RA Roth G.J.;  
 RA "Cloning of the alpha chain of human platelet glycoprotein Ib, a  
 transmembrane protein, with homology to leucine-rich alpha 2-  
 glycoprotein."  
 RT Proc. Natl. Acad. Sci. U.S.A. 84:5615-5619(1987).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=84025874; PubMed=2845078.  
 RA Weener R.H., Kieffer N., Wieki A.N., Clementson K.J.;  
 RA "Structure of the human blood platelet membrane glycoprotein Ib alpha  
 gene."  
 RT Proc. Natl. Acad. Sci. U.S.A. 84:5610-5614(1987)  
 RN [3]  
 RP Biochem Biophys Res Commun 156:484-486(1988).  
 RN [4]  
 RP SEQUENCE OF 17-315.  
 RX MEDLINE=87289654; PubMed=3427302.  
 RA Titani K., Takio K., Honda M., Ruggeri Z.M.;  
 RA "Amino acid sequence of the von Willebrand factor-binding domain of  
 platelet membrane glycoprotein Ib."  
 RT Proc. Natl. Acad. Sci. U.S.A. 84:5610-5614(1987)  
 RN [5]  
 RP DISULFIDE BONDS.  
 RX MEDLINE=91301149; PubMed=2070794.  
 RA Hess D., Schaller J., Rickli F.E., Clementson K.J.;  
 RA "Identification of the disulfide bonds in human platelet  
 glycoprotein Ib."  
 RT Eur. J. Biochem 199:389-394(1991)

BN [5]  
 RP VARIANT SIBA.  
 RX MEDLINE=92255598; PubMed=1586750.  
 RA Murata M., Furihata K., Ishida F., Russell S.R., Ware J.,  
 RA Ruggeri Z.M.;  
 RA "Genetic and structural characterization of an amino acid dimorphism  
 in glycoprotein Ib alpha involved in platelet transfusion  
 refractoriness."  
 RT Blood 79:3086-3090(1992).  
 BN [6]  
 RP VARIANT BSS PHE-73.  
 RX MEDLINE=92110577; PubMed=1730088.  
 RA Miller J.L., Lyle V.A., Cunningham D.;  
 RA "Mutation of leucine-57 to phenylalanine in a platelet glycoprotein  
 Ib alpha leucine tandem repeat occurring in patients with an  
 autosomal dominant variant of Bernard-Soulier disease."  
 RT Blood 79:439-446(1992).  
 BN [7]  
 RP VARIANT BSS VAL-172.  
 RX MEDLINE=93388851; PubMed=7690774.  
 RA Ware J., Russell S.P., Marchese P., Murata M., Mazzucato M.,  
 RA de Marco L., Ruggeri Z.M.;  
 RA "Point mutation in a leucine rich repeat of platelet glycoprotein Ib  
 alpha resulting in the Bernard-Soulier syndrome."  
 RT J. Clin. Invest 92:1213-1220(1993).  
 BN [8]  
 RP VARIANT BSS SEP-225.  
 RX MEDLINE=95118882; PubMed=7819107.  
 RA Sinsek S., Norris P., Lozano M., Pico M., von Dem Borne A.E.G.K.,  
 RA Pibera A., Gallardo D.;  
 RA "Cys209 Ser mutation in the platelet membrane glycoprotein Ib alpha  
 gene is associated with Bernard-Soulier syndrome."  
 RT Br. J. Haematol. 88:839-844(1994).  
 BN [9]  
 RP VARIANT PSEUDO-VWD VAL-249.  
 RX MEDLINE=91271273; PubMed=2052556.  
 RA Miller J.L., Cunningham D., Lyle V.A., Finch C.N.;  
 RA "Mutation in the gene encoding the alpha chain of platelet  
 glycoprotein Ib in platelet-type von Willebrand disease."  
 RT Proc. Natl. Acad. Sci. U.S.A. 88:4761-4765(1991).  
 BN [10]  
 RP VARIANT PSEUDO-VWD VAL-249.  
 RX MEDLINE=95253059; PubMed=8486780.  
 RA Murata M., Russell S.R., Ruggeri Z.M., Ware J.;  
 RA "Expression of the phenotypic abnormality of platelet-type von  
 Willebrand disease in a recombinant glycoprotein Ib alpha fragment."  
 RT Clin. Invest 91:2133-2137(1993).  
 BN [11]  
 RP VARIANT PSEUDO-VWD VAL-255.  
 RX MEDLINE=93214031; PubMed=8384898.  
 RA Russell S.D., Roth G.J.;  
 RA "Pseudo-von Willebrand disease: a mutation in the platelet  
 glycoprotein Ib alpha gene associated with a hyperactive surface  
 receptor."  
 RT Blood 81:1747-1751(1993).  
 BN [12]  
 RP VARIANT BSS LEU-195 DEL.  
 RX MEDLINE=95178321; PubMed=7873390.  
 RA de la Salle C., Paas M.-J., Lanza F., Schwartz A., Haudou D.,  
 RA Chevalier J., Gache C., Briquet M.-E., Cazenave J.-P.;  
 RA "A three-base deletion removing a leucine residue in a leucine-rich  
 repeat of platelet glycoprotein Ib alpha associated with a variant of  
 Bernard-Soulier syndrome (Nancy 1)."  
 RT Br. J. Haematol. 88:486-496(1995).  
 CC [1]  
 CC FUNCTION: gp-IR, A SURFACE MEMBRANE PROTEIN OF PLATELETS,  
 PARTICIPATES IN THE FORMATION OF PLATELET PLUGS BY BINDING TO VON  
 WILLEBRAND FACTOR, WHICH IS ALREADY BOUND TO THE SUBENDOTHELIUM.  
 CC [2]  
 CC SUBUNIT: GP-IR ALPHA AND BETA ARE DISULFIDE LINKED. GP-IX IS  
 COMPLEXED WITH THE GP-IR HETEROOLIGOMER VIA A NON COVALENT LINKAGE.  
 CC [3]  
 CC SURFACIAL LOCATION: Type I membrane protein.  
 CC [4]  
 CC PTM: GLYCOSYLATION, WHICH IS APPROXIMATELY COEXTENSIVE WITH THE  
 EXTRACELLULAR PART OF THE MOLECULE, IS CLEAVED OFF BY CALPAIN  
 DURING PLATELET LYSIS.

CC -1- POLYMORPHISM: POSITION 161 IS ASSOCIATED WITH PLATELET-SPECIFIC  
 CC ALLANTOGEN SIDE. SIDA: / HAN: LRR (2); AML: SARA (3) HAS MED: 161.  
 CC SIDA IS INVOLVED IN NEONATAL ALLOIMMUNE THROMBOCYTOPENIA (NATP).  
 CC -1- DISEASE: DEFECTS IN GPIIb/IIIa ARE ONE OF THE CAUSES OF BERNARD-SOULIER  
 CC SYNDROME (BSS). BSS PATIENTS HAVE UNUSUALLY LARGE PLATELETS AND  
 CC HAVE A CLINICAL BLEEDING TENDENCY.  
 CC -1- DISEASE: DEFECTS IN GPIIb/IIIa ARE ONE OF THE CAUSES OF VON WILLEBRAND  
 CC DISEASE (VWD). KNOWN AS PLATELET-TYPE VON WILLEBRAND DISEASE OR  
 CC PSEUDO-VON WILLEBRAND DISEASE. THIS AUTOSOMAL DOMINANT BLEEDING  
 CC DISORDER IS CAUSED BY AN INCREASED AFFINITY OF GPIIb/IIIa FOR SOLUBLE  
 CC VWF RESULTING IN IMPAIRED PROSTAGLANDIN PRODUCTION DUE TO THE REMOVAL  
 CC OF VWF FROM THE CIRCULATION.  
 CC -1- MISCELLANEOUS: PLATELET ACTIVATION APPARENTLY INVOLVES DISRUPTION  
 CC OF THE MACROMOLECULAR COMPLEX OF GPIIb/IIIa WITH THE PLATELET  
 CC GLYCOPROTEIN IX (CD-1X) AND DISSOCIATION OF GPIIb FROM THE  
 CC ACTIN-BINDING PROTEIN  
 CC -1- MISCELLANEOUS: BINDING SITES FOR VON WILLEBRAND FACTOR AND  
 CC THROMBIN (THE LATTER SITE WITH OPEN-WE POSITION) ARE IN THE  
 CC AMINO-TERMINAL PART OF THE MOLECULE.  
 CC -1- SIMILARITY: CONTAINS 6 LEUCINE-RICH REGIONS (LRR).  
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 CC EMBL: 202940; AAA52595.1;  
 CC EMBL: M22403; AAA52596.1;  
 CC PIR: A27075; NBUJIA.  
 CC GlycoSuiteDB: P07359;  
 CC MIR: 231200;  
 CC MIN: 177820;  
 CC InterPro: IPR001611; LRR;  
 CC InterPro: IPR000483; LRR\_Cterm;  
 CC InterPro: IPR000372; LRR\_Hterm;  
 CC InterPro: IPR003592; LRR\_Out;  
 CC InterPro: IPR003643; LRR\_YF;  
 CC Pfam: PF00560; LRR; 6;  
 CC Pfam: PF01463; LRRCT; 1;  
 CC Pfam: PF01462; LRRNT; 1;  
 CC PRINTS: PK00319; LRR\_Cterm;  
 CC SMART: SM00370; LRR; 3;  
 CC SMART: SM00092; LRRCT; 1;  
 CC SMART: SM00013; LRRNT; 1;  
 CC SMART: SM00469; LRR\_TYF; 2;  
 CC Platelet; Transmembrane; Glycoprotein; Hemostasis; Blood coagulation;  
 CC Popoel; Leucine rich repeat; Signal; Cell adhesion; Disease mutation;  
 CC Polymorphism; von Willebrand disease; Bernard Soulier syndrome.  
 CC  
 CC SIGNAL: 1 16  
 CC CHAIN: 17 626 PLATELET GLYCOPROTEIN IIB ALPHA CHAIN.  
 CC CHAIN: 17 7 ?  
 CC DOMAIN: 17 505 GLYCOCALICIN.  
 CC TRANSMEM: 506 526 EXTRACELLULAR (POTENTIAL).  
 CC DOMAIN: 527 626 POTENTIAL.  
 CC REPEAT: 70 92 CYTOPLASMIC (POTENTIAL).  
 CC REPEAT: 93 117 LRR 1.  
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 CC REPEAT: 8890 8910

DE Insulin-like growth factor binding protein complex acid labile chain  
DE precursor (ALS).  
GN IGFALS OR ALS.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=93038676; PubMed=1384485;  
RA Dai J., Baxter P.C.;  
RT "Molecular cloning of the acid-labile subunit of the rat insulin-like  
PT growth factor binding protein complex.";  
PL Biochem. Biophys. Res. Commun. 184:404-409(1992).  
RN [2]  
RP SEQUENCE OF 24-44, AND CHARACTERIZATION.  
RC STRAIN=Wistar; TISSUE=Serum;  
RX MEDLINE=94130835; PubMed=7507839;  
RA Baxter K.C., Dai J.;  
RT "Purification and characterization of the acid labile subunit of rat  
PT serum insulin-like growth factor binding protein complex.";  
PL Endocrinology 134:848-852(1994).  
CC -1- FUNCTION: MAY HAVE AN IMPORTANT ROLE IN REGULATING THE ACCESS OF  
CC CIRCULATING IGFs TO THE TISSUES.  
CC -1- SUBUNIT: FORMS A TERNARY COMPLEX OF ABOUT 140 TO 150 kDa WITH  
CC IGF-1 OR IGF-II AND IGF-RP-4  
CC -1- SUBCELLULAR LOCATION: Extracellular.  
CC -1- TISSUE SPECIFICITY: BRAIN, KIDNEY, LUNG, HEART, SPLEEN, MUSCLE  
CC AND LIVER.  
CC -1- SIMILARITY: CONTAINS 21 LEUCINE-RICH REPEATS (LRR).  
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DR EMBL: S46785; AAC02770.2;  
DR PIR: J01282; J01282.  
DR HSSP: P23945; LXUN.  
DR InterPro: IPR001611; LRR.  
DR InterPro: IPR000483; LRR\_Gterm.  
DR InterPro: IPR000372; LRR\_Nterm.  
DR InterPro: IPR003592; LRR\_out.  
DR InterPro: IPR003591; LRR\_type.  
DR Pfam: PF00360; LRR\_19.  
DR Pfam: PF01463; LRRCT; 1.  
DR Pfam: PF01462; LRRNT; 1.  
DR PRINTS: PR00019; LEUCICHRPT.  
DR SMART: SM00370; LRR; 5.  
DR SMART: SM00082; LRRCT; 1.  
DR SMART: SM00013; LRRNT; 1.  
DR SMART: SM00369; LRR\_TYP; 9.  
KW Glycoprotein; Leucine-rich repeat; Repeat; Signal.  
FT SIGNAL 1 23  
FT CHAIN 24 603 INSULIN-LIKE GROWTH FACTOR BINDING  
FT PROTEIN COMPLEX ACID LABILE CHAIN.  
FT REPEAT 52 73  
FT REPEAT 74 96  
FT REPEAT 98 120  
FT REPEAT 121 144  
FT REPEAT 146 168  
FT REPEAT 169 192  
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FT CARBOHYD 9919 9938  
FT CARBOHYD 9938 9957  
FT CARBOHYD 9957 9976  
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FT CARBOHYD 9995 10000

RESULT 6

ALS\_MOUSE

ID ALS\_MOUSE

AC P70489

DT 01-NOV-1997 (REL. 35, Created)

DT 01-NOV-1997 (REL. 35, Last sequence update)

DT 01-MAR-2002 (REL. 41, Last annotation update)

DE Insulin-like growth factor binding protein complex acid labile chain

DE precursor (ALS).

GN IGFALS OR ALS OR ALBS.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=129/SV.

RX MEDLINE=96413591; PubMed=8816745;

RA Borsella Y.R., Soto D., Hsieh S., Horst K.R., Goh G.T.

RT mouse acid labile subunit of the insulin-like growth factor binding

RT complex.";

RL Proc. Natl. Acad. Sci. U.S.A. 92:10028-10033(1995).

CC -1- FUNCTION: MAY HAVE AN IMPORTANT ROLE IN REGULATING THE ACCESS OF

CC CIRCULATING IGFs TO THE TISSUES.

CC -1- SUBUNIT: FORMS A TERNARY COMPLEX OF ABOUT 140 TO 150 kDa WITH

CC IGF-1 OR IGF-II AND IGF-RP-4 (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: Extracellular.

CC -1- SIMILARITY: CONTAINS 21 LEUCINE-RICH REPEATS (LRR).

CC











DB 115 NQLEVLVSWLGRKATGHIDLSNBRUKPPGGLANFTLLKLDGNCZETITLPOLLR 174  
 QY 162 GIPGTRPLRIACN-----TPITAQPPENACLAALQELVSN 198  
 DB 175 GPQLERLRIHFNKNKIQVIRKDLIPQPLPYVETNENKLPVAAAGAPGGLQELLMILSN 234  
 QY 195 ISLQALEF-----ELSSFFPEPLALAAAPNPNVPLSWSPGPPVRES 241  
 DB 235 NLSASVPEGLKASLSTQHWLWMLHCHLSS-----NWVLTGSLSSVYFVWZLA 247  
 QY 242 HVTIASPEETROHFFPKRAGLELL 265  
 DB 283 KFMFSSQNLTPCAQIDAVKQSL 306

RESULT 11  
 GPV\_HUMAN STANDARD: PPT: 560 AA  
 ID GPV\_HUMAN  
 AC 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Platelet glycoprotein V precursor (GPV) (CD42b).  
 GN GP5.  
 OS Homo sapiens (Human)  
 OC Eukaryota, Metazoa, Chordata, Craniota, Vertebrata, Euteleostomi,  
 OC Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.  
 OX NCBI\_TaxID=9606.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lung;  
 RA MEDLINE=93391348; PubMed=7690959;  
 RA Hickoy M.J., Eagen P.S., Yagi M., Roth G.J.;  
 FT "Human labeled glycoprotein V: characterization of the polypeptide  
 RT and the related Ib-V-IX receptor system of adhesive, leucine-rich  
 RT glycoproteins.";  
 PI Proc Natl Acad Sci U S A 90:8307-8311(1993)  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Platelet;  
 RX MEDLINE=94012616; PubMed=8407908;  
 RA Lanza F., Morales M., de la Salle C., Carretero I., Clementson K.J.,  
 RA Shimomura T., Phillips D.P.;  
 FT "Cloning and characterization of the gene encoding the human platelet  
 RT glycoprotein V. A member of the leucine-rich glycoprotein family,  
 RT cleaved during thrombin induced platelet activation";  
 RA J. Biol. Chem. 268:20801-20807(1993)  
 RN [3]  
 RP PARTIAL SEQUENCE.  
 RC TISSUE=Platelet;  
 RX MEDLINE=9478294; PubMed=2507000;  
 RA Shimomura T., Fujimura K., Maehana S., Takemoto M., Oda K.,  
 RA Fujimoto T., Oyama Y., Suzuki M., Teihara Tanaka K., Titani K.,  
 RA Kuramoto A.;  
 FT "Purification and characterization of human platelet  
 RT glycoprotein V: the amino acid sequence contains leucine-rich  
 RT repeat-like modules as in glycoprotein Ib.";  
 RA Blood 75:2447-2456(1990)  
 RN [4]  
 RP PARTIAL SEQUENCE.  
 RC TISSUE=Platelet;  
 RX MEDLINE=9531225; PubMed=2572284;  
 RA Pech G.L., Church T.A., McMullen B.A., Williams S.A.;  
 FT "Human platelet glycoprotein V: a surface leucine-rich glycoprotein  
 RT related to adhesion.";  
 RA Biochem. Biophys. Res. Commun. 170:153-161(1990)  
 CC -!- FUNCTION: THE GPIIb-IIIa COMPLEX FUNCTIONS AS THE VON WILLEBRAND  
 CC FACTOR RECEPTOR AND MEDIATES VON WILLEBRAND FACTOR-DEPENDENT  
 CC PLATELET ADHESION TO BLOOD VESSELS. THE ADHESION OF PLATELETS TO  
 CC INTURBED VASCULAR SURFACES IN THE ARTERIAL CIRCULATION IS A  
 CC CRITICAL INITIATING EVENT IN HEMOSTASIS.  
 CC -!- SURFACELLULAR LOCATION: TYPE I membrane protein.

-!- TISSUE SPECIFICITY: PLATELETS AND MEGAKARYOCYTES.  
 -!- PIM: THE N-TERMINUS IS BLOCKED.  
 -!- SIMILARITY: CONTAINS 14 LEUCINE-RICH REPEATS (LRR).  
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 EMBL: L11238; AAA03069.1; -;  
 EMBL: Z4393; CAA92637.1; -;  
 HSSP: P16473; 1XDM.  
 MIM: 173511; -;  
 InterPro: IPR001611; LRR.  
 InterPro: IPR000483; LRR\_Cterm.  
 InterPro: IPR000372; LRR\_Nterm.  
 InterPro: IPR003592; LRR\_out.  
 InterPro: IPR003591; LRR\_Lyp.  
 Pfam: PF00560; LRR; 14;  
 Pfam: PF01463; LRRCT; 1;  
 PRINTS: PR00019; DEBRICHPT.  
 SMART: SM00370; LRR; 1;  
 SMART: SM00062; LRRCT; 1;  
 SMART: SM00013; LRRNT; 1;  
 SMART: SM00369; LRR\_TYP; 9;  
 KW Platelet, Transmembrane, Glycoprotein, Blood coagulation;  
 KW Repeat; Leucine-rich repeat; Cell adhesion; Signal.  
 FT SIGNAL 1 16  
 FT CHAIN 17 560  
 FT DOMAIN 17 523  
 FT TRANSHEM 524 544  
 FT TRANSHEM 545 553  
 FT REPEAT 73 96  
 FT REPEAT 97 120  
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QY 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
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Db 187 RGIHICAGAKT EPIIIRNSFLVSDLSGELNSLCATELGFENHIRETAFZAFERFNLS 245
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QY 164 111 111 111 111 111 111 111 111 111 111 111 111 111 111
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QY 197 111 111 111 111 111 111 111 111 111 111 111 111 111 111
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Db 367 1VSLRNKRLALPALKFNLSLSSVLIHQHLELLPDGVSALPRLTEVLHINSWKD 426
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QY 288 1VVRPRLASSLAPTWLSPATAPAEPSSTAPTVGP 327
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Db 479 1P-PRPADSS-----KAPVHALPANSSEP 503
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RESULT 12  
CBP8 HUMAN

ID	ORGANISM	STANDARD	PRT	536 AA
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BJ				
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BV				
BW				
BX				
BY				
BZ				
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CC				
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FP				
FQ				















RESULT 3  
Q9HBM1 PRELIMINARY: PRT: 653 AA  
AC Q9HBM1  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE BRAIN TUMOR ASSOCIATED PROTEIN NAG14.  
GN NAG14.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN 1  
RP SEQUENCE FROM N.A.  
RA Wang J., Bin L., Jiang N., Li G.  
RT "Homo sapiens brain specific gene (PAC), downregulated in brain tumor,  
mRNA".  
SB Submitter (JUN-2001) to the EMBL/GenBank/CCDS databases.  
FMBL: AF196976; AAG28019.2;  
HSP: P23945; IJUN.  
DR InterPro: IPR003599; Ig.  
DR InterPro: IPR003598; Ig\_G2.  
DR InterPro: IPR003605; Ig\_Like.  
DR InterPro: IPR003606; Ig\_Like.  
DR InterPro: IPR003605; Ig\_Like.  
DR InterPro: IPR001611; LRR.  
DR InterPro: IPR000483; LRR\_Term.  
DR InterPro: IPR000372; LRR\_Nterm.  
DR InterPro: IPR003592; LRR\_Out.  
DR InterPro: IPR003591; LRR\_Typ.  
DR Pfam: PF00047; Ig\_1.  
DR Pfam: PF00560; LRR\_8.  
DR Pfam: PF01463; LRRCT\_1.  
DR Pfam: PF01462; LRRNT\_1.  
DR SMART: SM00409; IG\_1.  
DR SMART: SM00408; IG\_2; 1.  
DR SMART: SM00410; IG\_Like; 1.  
DR SMART: SM00370; LRR\_3.  
DR SMART: SM00042; LRRCT\_1.  
DR SMART: SM00013; LRRNT\_1.  
DR SMART: SM00369; LRR\_Typ; 7.  
KW Immunoglobulin domain.  
SQ SEQUENCE 653 AA; 72717 MW; 38150CHIF6850E37 CFC64;

Query Match 10.5%; Score 330; DB 4; Length 653;  
Best Local Similarity 24.3%; Pred. No. 1.4e-15;  
Matches 159; Conservation 82; Mismatches 245; Indels 169; Gaps 25;

QY 7 LLLPLLLL-----LALGPGVGGPSCGCS-QPQIVPCTAPGCTIVPRVDPD 53  
DB 17 ILLEFVYLIAQWILCAALAAASAGPQNP-PSW-SQNP-SKVVTAPGCTIVPRVDPD 76  
QY 54 TVRLVVFENGITMI DASSPAGIPGILINSONGLASLP-----LPRLLLDLSHNSLL 107  
DB 77 TRYLNLMNNIQLQATPPIHLEVLVLGLGPNSSPQIVGAFNGLASLNTLEFDNWL 136  
QY 108 ALPGCLIDTAN-----VEALRIAGLG-----LQQLDRGLSPILP 141  
DB 137 VIPSGAFYLSKLPFLWLPNNPTESTIPSYAFNPVPSLPLDLGLKFLYISCAPEGLF 196  
QY 142 N-----LHLDVSDNQLFV-PPVIVLGLCLPLPLAGNTPA 178  
DB 197 NKYINLGMNKNKMPNTPDLVLEELMSGNHIPETPGSPHLSLKKLWYN-NSQS 255  
QY 179 QLRFTETAGLAALQETAVSNLSLALPGLSLPPEPFIHAAA PGLFNWERSWEG 255  
DB 256 LIERNAFDGLASLVELLNHNHNSLPHD---LFTPLPYLVLELHHPNWCDCDILWLA 312  
QY 236 PWDFSHVTTASPEETCHPPKNAKPIILFIYVANGGQATTATVTPTTPVWPEPTA 295

DB 313 WMIPE-YIPNSTCCGPGCHAPMHMPGPYLVFVQASFCSSA-----PFIMVAPRINT 364  
QY 296 LSSSLAPTWISPTAPATRAPSPSTAPPTVGP-----VPQPDQCPSTCLNGTCHLGRH 351  
DB 365 SECPMA-----ELKQRTIPMSVSKWLLPNGTIVLASHAPPRISVLNDGT--LNESH 413  
QY 352 HLAQVDFPFGHGLYTESMGGTIPSTIVHPPHPS-IPSTFVSPSS; PWTGQYLGQ 411  
DB 414 VLG SLTVY TGVTVVAGRL NASAYLIV 441  
QY 412 SEVQLSELELYPNLSCHFEPLVTLRLASLAAYIVTLGRNATYSVVMPP----- 462  
DB 442 STAEINISWSET - IVTVETTESPEETETKFKVFTTSTGVCFAITSTIVL 494  
QY 463 LGFGKVFCEACGEARHTTAVHSHNIAFVQAKENLLELLAFALAAVLLAAAVCAAY 522  
DB 495 LGTRVPR-QVAVPATDITDKMUTSLDEVMKTK-----ITGCVAVVILLAAAMLVFP 548  
QY 523 QVGR---GRMAAAAKQKQVQVZAPLPIPLPQVFPVPPGPKATPGGGEALPSG 573  
DB 549 KLPKPHQGGSTVIAAV-----VPIIQVQ-EDIPAAISMAAIAAFSG 589  
RESULT 4  
Q96A85  
ID Q96A85 I-PELIMINAKY; PRI: 54% AA.  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE HYPOTHETICAL 72.3 KDA PROTEIN.  
GN BAG.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN 1  
RP SEQUENCE FROM N.A.  
RA Wang J.;  
RT Thesis (2000), Shenshan Medical University, Guangzhou, China.  
DE EMBL: AJ297858; CAC82651.1;  
KW Signal; Hypothetical protein.  
FT SIGNAL 38 POTENTIAL.  
SQ SEQUENCE 649 AA; 72313 MW; 9C11C5ABC7E536CF CRC64;

Query Match 10.5%; Score 329; DB 4; Length 649;  
Best Local Similarity 24.6%; Pred. No. 1.6e-15;  
Matches 159; Conservation 81; Mismatches 247; Indels 177; Gaps 25;

QY 7 LLLPLLLL-----LALGPGVGGPSCGCS-QPQIVPCTAPGCTIVPRVDPD 53  
DB 17 ILLEFVYLIAQWILCAALAAASAGPQNP-PSW-SQNP-SKVVTAPGCTIVPRVDPD 76  
QY 54 TVRLVVFENGITMI DASSPAGIPGILINSONGLASLP-----LPRLLLDLSHNSLL 107  
DB 77 TRYLNLMNNIQLQATPPIHLEVLVLGLGPNSSPQIVGAFNGLASLNTLEFDNWL 136  
QY 108 ALPGCLIDTAN-----VEALRIAGLG-----LQQLDRGLSPILP 141  
DB 137 VIPSGAFYLSKLPFLWLPNNPTESTIPSYAFNPVPSLPLDLGLKFLYISCAPEGLF 196  
QY 142 N-----LHLDVSDNQLFV-PPVIVLGLCLPLPLAGNTPA 178  
DB 197 NKYINLGMNKNKMPNTPDLVLEELMSGNHIPETPGSPHLSLKKLWYN-NSQS 254  
QY 183 EDLAGLAALQETAVSNLSLALPGLSLPPEPFIHAAA PGLFNWERSWEG 238  
DB 255 LIERNAFDGLASLVELLNHNHNSLPHD---LFTPLPYLVLELHHPNWCDCDILWLA 311  
QY 239 PWDFSHVTTASPEETCHPPKNAKPIILFIYVANGGQATTATVTPTTPVWPEPTA 298  
DB 312 PE-YIPNSTCCGPGCHAPMHMPGPYLVFVQASFCSSA-----PFIMVAPRINT 363

QY 299 SLAPTWLSTAPATAPAPSPSTAPPTGVP VEQDQDPPSTCLNGCHLCTRHLA 354  
 DB 364 RMA-----ELKORTPPMSSWKLLPNCITVLSHSHRPRI SVLNDGT--LNFSHVLL 412  
 QY 355 CUCPEFTSLYCESMGQETMSPTPTVTPRPRSLTLCIEPVSPTSLSKVLGLQRYLOGSSV 414  
 DB 413 -----SDTGVY-----TCWTVNAGNS--NASAYLVNSTA 440  
 QY 415 QLSRLILYRNISGDKKRLVLRIPASIAHYTVTOLRPNATYSVCMPT-----LCP 465  
 DB 441 ELNYSNPSPT-----TVVETTESPEDTTRKYPVPVPTTSGYQPAVYTTSTVLIQT 493  
 QY 466 GVPPECFEACGEAHTPPAVHSHNAPVTCAPESNPLLIAPALAAVLLAALAAVGAAYCVR 525  
 DB 494 TRVPC-QVAVPAIDITDKMQLSGLVEMKTK-----IIIGCFVAVTLLAAMLIIVFKLR 547  
 QY 526 R---GRAMAAAQKGVGPGAGPLERGVAVPLEPGPKATPGRGSEALPSG 573  
 DB 548 KHLQKSTVTAAR-----TVETIQVD-EDIPAATSAATAAPSG 585

RESULT 5  
 ID 075139 PRELIMINARY; PPT; 811 AA  
 AC 075139;  
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
 DE KIA00544 PROTEIN.  
 GN KIA00544.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 OX NCBI\_TaxID:9606;  
 RN 1  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-BRAIN;  
 RA Ishikawa K., Nadase T., Suyama M., Miyajima N., Tanaka A., Kotani H.,  
 RA Nomura N., Ohara O.  
 RT "Prediction of the coding sequences of unidentified human genes. X.  
 RT The complete sequences of 106 new cDNA clones from brain which can  
 RT code for large proteins in vitro."  
 RL DNA Pos. 5,160-176(1998)  
 RE EMBL; AB014544; BAA31619.1;  
 DB InterPro; IPR001611; LRR.  
 DB InterPro; IPR000483; LRR\_Cterm.  
 DB InterPro; IPR000372; LRR\_Nterm.  
 DB InterPro; IPR003394; LRR\_Typ.  
 DB Pfam; PF00560; LRR; 10.  
 DB PRINTS; PR001463; LRRCT; 1.  
 DB SMART; SM00082; LRRCT; 1.  
 DB SMART; SM00013; LRRNT; 1.  
 DB SMART; SM00369; LRR\_Typ; 10.  
 SQ SEQUENCE 811 AA; 88695 MW; 57410766ARK75F7R (nr64);

Query Match 10.3% Score 322.5, DB 4; Length 811;  
 Best Local Similarity 22.08; Pred. NC. 6.3e-15;  
 Matches 184; Conservative 62; Mismatches 272; Indels 317; Gaps 28,  
 QY 7 LLLPLLLALLADPNVGG-CYSGTGA-SQGVCTVETAPAGTITVPR----FVPPGVTVGVVEF 61  
 DB 9 LLLVVG-LAUPPLAEPV-PEKTLAQHPQLHLLTNKPLRVVPKLSLPSHPLVLSLQ 68  
 QY 62 NGITMLDASSAGLGLGLLLDSNQASL-----RLPRLLLDLSHNSLALERGLLD 115  
 DB 69 NPTNITAFDRHRVQPIQLQVNYQNTKSLHPKTFEKLSEIFVYIGNNLLQALAPGTLA 128  
 QY 116 T----- 116

DB 129 PLKRLILLYANENELSKLSGSGFESLVSFLKGNALGALPIAVAPALONLILYHLES 188  
 QY 117 -----ANVEATRLAGLQLOLDDEGL-----PSRI RNIHDIIVSNOLERY 156  
 DB 189 NPITPLGNATAQCKIPFENISANFQPSIPIAAATEADPTPSLSLITISANSIQHIDPR 248  
 QY 157 -----PPVLRGLRGLTRKLACN----- 174  
 DB 249 FCHI DRI GII SI PQNTI THI APFAFWI FAF PPI RFGNRI SQLPTALDELRLSLALDL 308  
 QY 175 --TRIAAGPEPLAGLAALAELEYSNI SI AALPEGLSCLTPPIPIIAAANDPNTVTP 231  
 DB 309 SGNELSAIHATFCHGLRPLPELSLNNALSAISGLIPAAAPALYPLDLPNGNWLTPKLR 368  
 QY 232 -- SWFCWVRESIVT LASPEETKECHFFPKNCKLLELDYAD-----PGTATTTAT 282  
 DB 369 GIKRMGQWHSQGRLLTVF--VQCRHHPALRGKY--LDYLDQQQLQNGSCALPSSAS 422  
 QY 283 VPTTRPVVREPTALSSSLAP-----TW----- 404  
 DB 423 LTADRRROPLTTAAGEEMTPPAGLAHELPPQQLQOORFLAGVAMKAAKELVGNKSL 482  
 QY 305 -LSPIATATEAPSPSTAPPTVGVFVPOPOKCPSPSLTGLNGGCTCHIGTRHLLACLPAGETG 463  
 DB 483 ELSPRPGGLQGPSVA--AAGDAPQSLD----- 510  
 QY 364 LYCESMGQGLIKPSHLPVLPKPSLILGIEFVS-----PTSLRVGLORY----- 408  
 DB 511 DEKKEQCEPTTAQALAEPTIPASPSAISPAQIPWGPATKKRGLRGTHERKRAQNSHGA 570  
 QY 409 -----LQSSVQIESIRITYR-----LSDEKRYLTER 447  
 DB 571 ELPLVLSQCPENKFIENLVEAGALSA-VKVAVFHRSPLRPGARPIIFDRPDQO 640  
 QY 438 -----LPASLAETVTLQRPNATYSVCMPLGSRVPEGEACGPAHPIVAVSHHA 489  
 DB 631 PRHFVYLPSSDSATLRELGDTPLVLCVGVGLGRV-----C-----IVAPKIDIC 678  
 QY 490 D--VTOARFQN-----DPIIAPALAAVLAALAAVGAAYCVRGCHAMAAAQIKRQ 539  
 DB 679 ASLVILPLKAGSGVYQLLLALLVNAIVLIALAAWASQWLPKALVAPP 740  
 QY 540 VQVQAPGLELE---GVFWILE---PAPALPQSSGA-LP-GSEF---FVIMPTTP 584  
 DB 721 --KQZAPVWVPMYSTPPTPLPSMGLVSAFSPQSPSHPTPTVATLSEAQLSPD 783  
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 ID Q9BTN0 PRELIMINARY; PPT; 638 AA.  
 AC Q9BTN0;  
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE HYPOTHETICAL 66.3 KDA PROTEIN.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 OX NCBI\_TaxID:9606;  
 RN 111  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=LUNG CARCINOMA;  
 RA Strausberg R.  
 PL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
 DB EMBL; HC003578; AA003578.1;  
 DB InterPro; IPR004961; FN\_III.  
 DB InterPro; IPR003594; Iq.  
 DB InterPro; IPR003548; Iq\_C2.  
 DB InterPro; IPR004006; Iq\_MHC.  
 DB InterPro; IPR001611; LRR.  
 DB InterPro; IPR000483; LRR\_Cterm.  
 DB InterPro; IPR000372; LRR\_Nterm.  
 DB InterPro; IPR003594; LRR\_Typ.

DR Pfam: PF00041; fn3; 1.  
 DR Pfam: PF00047; ig; 1.  
 DR Pfam: PF00560; LP8; 6.  
 DR Pfam: PF01463; LRCT; 1.  
 DR PRINTS: PK00019; LEURICHRPT.  
 DR SMART: SM00060; FN3; 1.  
 DR SMART: SM00409; IG; 1.  
 DR SMART: SM00408; IG2; 1.  
 DR SMART: SM00082; LRCT; 1.  
 DR SMART: SM00013; LRNT; 1.  
 DR SMART: SM00464; LPP; 1.  
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 DR SMART: SM00464; LPP; 3.  
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 DR SMART: SM00464; LPP; 5.  
 DR SMART: SM00464; LPP; 6.  
 DR SMART: SM00464; LPP; 7.  
 DR SMART: SM00464; LPP; 8.  
 DR SMART: SM00464; LPP; 9.  
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 DR SMART: SM00464; LPP; 11.  
 DR SMART: SM00464; LPP; 12.  
 DR SMART: SM00464; LPP; 13.  
 DR SMART: SM00464; LPP; 14.  
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 DR SMART: SM00464; LPP; 93.  
 DR SMART: SM00464; LPP; 94.  
 DR SMART: SM00464; LPP; 95.  
 DR SMART: SM00464; LPP; 96.  
 DR SMART: SM00464; LPP; 97.  
 DR SMART: SM00464; LPP; 98.  
 DR SMART: SM00464; LPP; 99.  
 DR SMART: SM00464; LPP; 100.

Query Match 10.2%, Score 321, ID 4, Length 629.  
 Best Local Similarity 23.9%, Pred. No. 5, 9e-15;  
 Matches 163; Conservative 56; Mismatches 256; Identities 208; Gaps 25;

DR 8 LIPILL-LALGPG-----VGGPSGCG---SQDTVPTCTAPGCTTVMPDVPPTV 65  
 DB 3 ILPLILLPLAPASSPQSTPSCPCPCPCPCPCPCPCPCPCPCPCPCPCPCPCPC 62  
 QY 56 GYVFNPTITMIPASSVACHTPCTVPTCTVPTCTVPTCTVPTCTVPTCTVPTCT 100  
 DB 63 ELRIADNFIASVRRDIANMTGLHLSLNTTHVAAGAFADPAFAHILHGNELSL 122  
 QY 101 -----LSNLSLLEPCIL--TANVEALPLAGLGLGLGLGLGLGLGLGLGL 144  
 DB 123 CQKQKGLVNRHIIISNGLAALAGATPCATHEGLSYNNLEQLFWALGLSNG 182  
 QY 144 HILVSDNCFEVPVPTCTVPTCTVPTCTVPTCTVPTCTVPTCTVPTCTVPTCT 204  
 DB 183 NTLGLDHLASVP-----AG-----APSLHLKRLMTSPLIT 218  
 QY 204 LPGLDGLPLRLLAAR-----NPPNCVCLSWPGVWRVSHVTLASPR 250  
 DB 219 LPDGLPL 269  
 QY 251 TRCHPPKAGLLELDYADRG-PATTTTATVPTTTRVVRPTALSSLA-----PT 403  
 DB 270 PACASFPALGGRYFWAGVEHVFCEPVVTHRSPLAVPAGR-PAALRCVAGDDPRVK 428  
 QY 304 WLSP-----TAP-----ATRAPSPSTAPTVGPVPO 430  
 DB 329 WVSQGLLGNSSRAAFENGITELLVTEPDGGLPTCIAAAGATAAVALTVGPVPP 388  
 QY 331 PQ-----DCPSTGLNGTCHGLKHLGLAGLCPGFTGLYCESOMGGTSPSTPTPR 385  
 DB 389 PGLANSICDPP-----DG-----DPDALTPS 412  
 QY 386 PRSLTGLLEPVSPTSLVGLQRYLQSSVGL-----RSLPLTYRNLSPDKRL 433  
 DB 413 AASASAKVADTGPTR GVGVTEGATAALVORPQRPPIGRMYQIQYN--SSADDL 469  
 QY 434 VTLRLPASLGYTTQLRPNATYVSVYPL-----GPRVPEGEAGEAHTPAVSHNIA 489  
 DB 470 YRMTPAESRFLTDLASGTYDLGLVAVENSATGLTATRPVGCARTSTEDALPQGA 529  
 QY 490 PVOQAREGNLPLIAPALAAVLAALAAVGAACVVRGR-----AMAAAADKQ 539  
 DB 530 PHAPLGTMTIATLGGVIVASVIFTEVILMPYKVGQGPGRKPIIAPVSSVCSQTNCA 589  
 QY 540 VARGAGPLEGVRVPLRPFKA 562  
 DB 590 LGPIPIP-----APPAPEFAA 605  
 RESULT 7  
 QYUGS3  
 ID QUGS3  
 AC QUGS3  
 DT 01-MAY-2000 (Tremblrel 14, Created)

DT 01-MAY-2000 (Tremblrel 13, Last sequence update)  
 DT 01-DEC-2001 (Tremblrel 19, Last annotation update)  
 DE 00756623.1 (NARL LUCINE RICH PROTEIN) (FRAGMENT)  
 GN 00756623.1.  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Mammalia; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 CX NCBI\_TaxID:9606;  
 RN 11  
 RP SEQUENCE FROM N.A.  
 PA Corby N.;  
 FL 00756623.1 (AM 2001) 50,116,117,118,119,120,121,122,123,124,125,126,127,128,129,130,131,132,133,134,135,136,137,138,139,140,141,142,143,144,145,146,147,148,149,150,151,152,153,154,155,156,157,158,159,160,161,162,163,164,165,166,167,168,169,170,171,172,173,174,175,176,177,178,179,180,181,182,183,184,185,186,187,188,189,190,191,192,193,194,195,196,197,198,199,200,201,202,203,204,205,206,207,208,209,210,211,212,213,214,215,216,217,218,219,220,221,222,223,224,225,226,227,228,229,230,231,232,233,234,235,236,237,238,239,240,241,242,243,244,245,246,247,248,249,250,251,252,253,254,255,256,257,258,259,260,261,262,263,264,265,266,267,268,269,270,271,272,273,274,275,276,277,278,279,280,281,282,283,284,285,286,287,288,289,290,291,292,293,294,295,296,297,298,299,300,301,302,303,304,305,306,307,308,309,310,311,312,313,314,315,316,317,318,319,320,321,322,323,324,325,326,327,328,329,330,331,332,333,334,335,336,337,338,339,340,341,342,343,344,345,346,347,348,349,350,351,352,353,354,355,356,357,358,359,360,361,362,363,364,365,366,367,368,369,370,371,372,373,374,375,376,377,378,379,380,381,382,383,384,385,386,387,388,389,390,391,392,393,394,395,396,397,398,399,400,401,402,403,404,405,406,407,408,409,410,411,412,413,414,415,416,417,418,419,420,421,422,423,424,425,426,427,428,429,430,431,432,433,434,435,436,437,438,439,440,441,442,443,444,445,446,447,448,449,450,451,452,453,454,455,456,457,458,459,460,461,462,463,464,465,466,467,468,469,470,471,472,473,474,475,476,477,478,479,480,481,482,483,484,485,486,487,488,489,490,491,492,493,494,495,496,497,498,499,500,501,502,503,504,505,506,507,508,509,510,511,512,513,514,515,516,517,518,519,520,521,522,523,524,525,526,527,528,529,530,531,532,533,534,535,536,537,538,539,540,541,542,543,544,545,546,547,548,549,550,551,552,553,554,555,556,557,558,559,560,561,562,563,564,565,566,567,568,569,570,571,572,573,574,575,576,577,578,579,580,581,582,583,584,585,586,587,588,589,590,591,592,593,594,595,596,597,598,599,600,601,602,603,604,605,606,607,608,609,610,611,612,613,614,615,616,617,618,619,620,621,622,623,624,625,626,627,628,629,630,631,632,633,634,635,636,637,638,639,640,641,642,643,644,645,646,647,648,649,650,651,652,653,654,655,656,657,658,659,660,661,662,663,664,665,666,667,668,669,670,671,672,673,674,675,676,677,678,679,680,681,682,683,684,685,686,687,688,689,690,691,692,693,694,695,696,697,698,699,700,701,702,703,704,705,706,707,708,709,710,711,712,713,714,715,716,717,718,719,720,721,722,723,724,725,726,727,728,729,730,731,732,733,734,735,736,737,738,739,740,741,742,743,744,745,746,747,748,749,750,751,752,753,754,755,756,757,758,759,760,761,762,763,764,765,766,767,768,769,770,771,772,773,774,775,776,777,778,779,780,781,782,783,784,785,786,787,788,789,790,791,792,793,794,795,796,797,798,799,800,801,802,803,804,805,806,807,808,809,810,811,812,813,814,815,816,817,818,819,820,821,822,823,824,825,826,827,828,829,830,831,832,833,834,835,836,837,838,839,840,841,842,843,844,845,846,847,848,849,850,851,852,853,854,855,856,857,858,859,860,861,862,863,864,865,866,867,868,869,870,871,872,873,874,875,876,877,878,879,880,881,882,883,884,885,886,887,888,889,890,891,892,893,894,895,896,897,898,899,900,901,902,903,904,905,906,907,908,909,910,911,912,913,914,915,916,917,918,919,920,921,922,923,924,925,926,927,928,929,930,931,932,933,934,935,936,937,938,939,940,941,942,943,944,945,946,947,948,949,950,951,952,953,954,955,956,957,958,959,960,961,962,963,964,965,966,967,968,969,970,971,972,973,974,975,976,977,978,979,980,981,982,983,984,985,986,987,988,989,990,991,992,993,994,995,996,997,998,999,1000.  
 Query Match 10.2%, Score 421, ID 4, Length 797;  
 Best Local Similarity 25.5%, Pred. No. 7, 9e-15;  
 Matches 184; Conservative 67; Mismatches 296; Identities 204; Gaps 28;

QY 472 EFACGDAITPAPVNHAVT 75AGDNDLPLZATATAAVALAANVAAGVAFVLE- 526  
 DB 603 LGAGHARPEKFKTHDRNGKRPVDTGATFG-TPATLFGKSNPFPALRD-GAFQPVGRS 660  
 QY 527 -----CPAMAAAAGQGVGVVCAVPIPIFQVAVVIFQVPRKATEGGGALDSGRTD 577  
 DB 661 LQHLFLNNSGIEQICBAFSG-IGDQIQSHQKNGIPALP-----ALPSLSOLE 709  
 QY 578 V 578  
 DB 710 L 710

RESULT 8  
 QY 643155 PRELIMINARY: PRT: 660 AA.  
 AC 643155 (1-EMBLrel, 06, Created)  
 DT 01-JUN-1998 (1-EMBLrel, 06, Last sequence update)  
 DT 01-JUN-1998 (1-EMBLrel, 06, Last sequence update)  
 DT 01-DEC-2001 (1-EMBLrel, 19, Last annotation update)  
 DE K1AA0405 (1-EMBLrel, 06, REPEAT TRANSMEMBRANE PROTEIN PTPT2)  
 GN K1AA0405 OR FLRT2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Primates; Catarrhini; Hominoidea; Homo  
 OX NCBI\_TaxID:9606;  
 RN 11  
 RP SEQUENCE FROM N.A.  
 RA Ishikawa K., Nakase T., Nayaajima D., Seki N., Ohira M., Miyajima N.,  
 Tanaka A., Kotani H., Nomura N., Ohara O.,  
 Submitted (oct-1997) to the EMBL/GenBank/DDBJ databases.  
 RN 12  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE: 20112755; PubMed: 10444449.  
 RA Lacy S.E., Konemann C.G., Buzney E.A., Kunkel L.M.;  
 RT "Identification of FLRT1, FLRT2, and FLRT3: A Novel Family of  
 RT Transmembrane Leucine-Rich Repeat Proteins";  
 RL Genomics 62:417-426(1999).  
 DR EMBL: AB007865; BAA23701.1;  
 DR EMBL: AF164676; AAF28460.1;  
 DR InterPro: IPR004961; FN111.  
 DR InterPro: IPR001611; LRR  
 DR InterPro: IPR0000483; LRR\_Gterm.  
 DR InterPro: IPR000372; LRR\_Nterm.  
 DR InterPro: IPR003592; LRR\_out.  
 DR InterPro: IPR003591; LRR\_Typ.  
 DR InterPro: IPR001211; PIP\_A2.  
 DR Pfam: PF00041; In3; 1.  
 DR Pfam: PF00560; LRR; 9.  
 DR Pfam: PF01463; LRRCT; 1.  
 DR Pfam: PF01462; LRRNT; 1.  
 DR SMART: SM00370; LRR; 3.  
 DR SMART: SM00082; LRRCT; 1.  
 DR SMART: SM00143; LRRNT; 1.  
 DR SMART: SM00369; LRR\_Typ; 1.  
 DR PROSITE: PS00119; PA2\_A20; CHRMW\_1.  
 KW Transmembrane.  
 SQ SEQUENCE 660 AA: 74048 MW: 901523830056778 GRC64;

Query Match 10.2% Score 320, DB 4, Length 660.  
 Best Local Similarity 22.4% PctId: 60, 7.4e-15,  
 Matches 140; Conservative 87, Mismatches 216, Labels 182, Gaps 23;

QY 13 LLLALGQW-----GCPSPVWSPQVTFCTAPASTVTPDQVDPVSLVVF----- 60  
 DB 20 LLLSLGYSQVSKLLACVSCVCRDR-NFYWYNSRSLTSPGVTVIVHNNQINNA 78  
 QY 61 -----ENGLMLDLSAFGLQGLQL 81  
 DB 79 GFPAELHNVQSVHTVYVYGNQLDFPMNIPKNVPVHLHGFNNIQTISPAAALQLFLKEI 198

QY 82 ELSSQSTANSELF -----KLLLLLEHRLALEGG- LGSANVVALKA GL 127  
 DB 139 HLLNSISTVGVHGAFAREALSKLILFSLKNLSSVWGLVDFQLKVDENRITAVISDM 198  
 QY 228 GLSQLD-----EGLSEERERHCLAVSUSRELEEVVAVISELKEEL 169  
 DB 199 AFQNLTSLEPLVNGNLTNKGIAEGTESHLTKKEFSIVENSLSHPPDLPDTH-LIR 267  
 QY 170 PLAGNTELAGIPEHQAAGAAQQLIVVSHPTQALQGN 591 PDEPLIAAAPHDPVWV 229  
 DB 258 YLQEN-QIHUIPIQASNLKPTPTIENNGEEMITAEVTHIENIKQITAKRNWFGW 316  
 QY 239 PLSNFGVWVSHVILASTPEETRECHITPKNAELLELDYADNKPATITATVTHPV 289  
 DB 417 SKKVTFWIKVDSDD-NVSGEMQGGDFVGRMAYRFTNMNLSQD--TIIHGLFLFD 472  
 QY 290 VREPTALSSSLAPTSLSPATAPSPSPSTAPTVGVGPQPGVQWPPSPCTNCTCHLGT 439  
 DB 373 -----APST--ASPTQPTLS-IPNI-----S 492  
 QY 350 PHHACIQHPEPCHVYPSQMGCCGPPPP-----VPPPPRSITLIEP 495  
 DB 393 RSY-----TPPTTSKLTPTIDWCGREWVTFPISEFQLSHF 431  
 QY 404 VSPSTLPVQIERYTGLSSVQIPSLPIVTHNSPTKPIVTPLEPLASAFY-TVTOLENA 454  
 DB 432 VNDISQVSWLSIFVMAKLTWNGHSLVGG-----IVQRTVSGEKHLSVNLHRS 487  
 QY 455 TVSWVMPDPSGPPVPEEEA-CSEAHITPA-----VESNHIAVTEAPGNLPELLAPA 506  
 DB 488 TYRICLVPLDAFNAVEDPTICSEATTHIASVYNGSNTASSHEQTTSMSRS-PELLAGL 546  
 QY 507 LAAVLLAALAAVCAAYC---VRRGR 528  
 DB 547 TGGAVIFVAVLLSVFQWEMKEGR 571

RESULT 9  
 QY 90017 PRELIMINARY: PRT: 792 AA.  
 AC 90017  
 DT 01-MAY-2000 (1-EMBLrel, 13, Created)  
 DT 01-MAY-2000 (1-EMBLrel, 13, Last sequence update)  
 DT 01-DEC-2001 (1-EMBLrel, 19, Last annotation update)  
 DE WUGSC:H\_GSI65L15.2 PROTEIN (FRAGMENT).  
 GN WUGSC:H\_GSI65L15.2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 OX NCBI\_TaxID:9606;  
 RN 11  
 RP SEQUENCE FROM N.A.  
 RA Geisler C., Antoniou B., Angel S.;  
 RT "The sequence of Homo sapiens BAC clone GSI-165L15,"  
 EL Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.  
 RN 12  
 RP SEQUENCE FROM N.A.  
 RA Waterston R.;  
 DT Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL: AC005013; AAC79690.1;  
 DR InterPro: IPR001611; LRR.  
 DR InterPro: IPR000483; LRR\_Gterm.  
 DR InterPro: IPR000472; LRR\_Nterm.  
 DR InterPro: IPR003593; LRR\_Typ.  
 DR Pfam: PF00560; LRR; 10.  
 DR Pfam: PF01463; LRRCT; 1.  
 DR PRINTS: PR00019; LEURICHPPT.  
 DR SMART: SM00082; LRRCT; 1.  
 DR SMART: SM00143; LRRNT; 1.  
 DR SMART: SM00369; LRR\_Typ; 10.  
 DR NON\_TER  
 FT SEQUENCE 792 AA: 86656 MW: 1000084586870 GRC64;



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Db 526 KAETA-----DSYGETTLNQAGNAGMASDPLAGITIGGAVALVFLVLGALCWVYHOAG 581
QY 522 YCVPRGMAAAAGDKCQVPCACPLFLGCVKVPLEPCPKATEGGALPSCSGCEVPLM 581
Db 582 ELUTFPAYNPGSPR-----DYMESOTFKDNSIL 612
QY 582 GEPGGLQ-----SPLIAK 595
Db 613 EIKCPGLQMLPINDYRAK 630

RESULT 11
ID Q9P254 PRELIMINARY; PRT: 662 AA.
AC Q9P259;
DT 01-OCT-2000 (TREMBLrel 15, Created)
DT 01-OCT-2000 (TREMBLrel 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel 19, Last annotation update)
DE KIAA1469 PROTEIN (FRAGMENT).
DE KIAA1469.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN 11
RP SEQUENCE FROM N.A.
RX MEDLINE=20277482; PubMed=10819331;
RA Rappaport, Kikano, F., Ishikawa K., Hirokawa M., Ohata G.;
RT Prediction of the coding sequences of unidentified human
RT genes.XVII.The complete sequences of 100 new cDNA clones from brain
RT which code for large proteins in vitro.*;
PL ENA Acc. 7:143-150(2000).
DE EMBL: AB040902; BAA95993.1;
DR InterPro: IPR003961; FN_111.
DR InterPro: IPR001611; LRR.
DR InterPro: IPR000483; LRR_Gterm.
DR InterPro: IPR000372; LRR_Nterm.
DR InterPro: IPR003592; LRR_out.
DR InterPro: IPR003591; LRR_typ.
DR InterPro: IPR001211; PLP_A2.
DR Pfam: PF00041; fn3; 1.
DR Pfam: PF00560; LRR; 10.
DR Pfam: PF00560; LRR; 10.
DR Pfam: PF01463; LRRCT; 1.
DR Pfam: PF01462; LRRNT; 1.
DR Pfam: PF01462; LRRNT; 1.
DR SMART: SM00369; FN3; 1.
DR SMART: SM00370; LRR; 1.
DR SMART: SM00082; LRRCT; 1.
DR SMART: SM00013; LRRNT; 1.
DR SMART: SM00013; LRRNT; 1.
DR SMART: SM00369; LRR_TYP; 1.
SQ SEQUENCE 662 AA: 74459 MW: 87000.68444429 CPC64;

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Query Match 9.94, Score 309; DB 4, Length 662;
Best local similarity 22.99; Pred No 4,60-14.
Matches 146, Conservative 97, Mismatches 216, Indels 192, Gaps 27,

QY 2 GSAPVLLDLE-----LLALGP- GVAGTSSGTCGSCQIVVPLAHGL 44
Db 5 CTKSTLLTMSAAMSIFLGTGKLGFLQVAPLSVWAKSCPSVCH-(DAHIV)NQHPT 64
QY 45 TVPQWPPVIVIVPVPNTIMDASSPACIQ-----NNAGTFSLEKNIKVKRYLYHNSLDEFPINLPK 117
Db 64 SFTGPIEGATLLYLNQNJ-----RPPHLLIDYSHNSL--LALPGLITANTVAFPLACIG 129
QY 78 -LQIDLSNQIASI-----RPPHLLIDYSHNSL--LALPGLITANTVAFPLACIG 129
Db 118 YKAEHLQFNNTRTIYDLSKIPYIEFLHLDNDSVASVTEEGAFKSNY--LRLEFLS 175
QY 129 LQQLDGLFSPFNHIDVSNQKFPV-PVPIETPGLTETPLAGN----- 174

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Db 176 RNHLSTIPWCLPTEELFELGNPSTISSPSLGLSLKPLVLINLNNHGLKVFEE 235
QY 175 -----TRIAGLR-----PDLAG-----LAAQLFHLVSNLS 200
Db 235 NVNLTSLVPSNLTAAPVNLPGTNLPELYLQNEINFEVFNHASYLQLYPLDSSNN 295
QY 201 LQALPGDLSLFPPEPLTAAAPNPNVCTPSWPGFWPESUHTLASDELTHCHPENA 260
Db 296 LSNLPGTIFGLLINLIGLILKNNQWYQCKMAWPHIWIQSLPVKV-NVNGLMQVAPFVR 354
QY 261 GRLLLELDYADFCPATTTTATVPTTRVVRPEPTALSSSLAPTWSLPTADAFASPSST 320
Db 355 GMAIKDLNAELFDCKDSGIVSTIQIT-----TALPNTVYPAQGWAPVTKQPD----- 403
QY 321 APPTVAVTQPGCPPESTCTNGCTCHLGTPHHLAGLCPETGLCYCESQMGAGTSPSTP 380
Db 404 -----LKNPK-----LTKDR-----OTTCGFS 420
QY 381 VTEPFPS;TGTCTEFSPTSLKVLQGVYLGSSVGLRSRLTYPNLSGP-LKRLVTLRLP 439
Db 421 -----RKTITIVKSVTSDTIHLSMKLALPMTALRLSLWIKLCHSPAFGSLTETIVT----- 471
QY 440 ASGASVIVLIENATYSVTVMIIGGKRVFEGF ACQPAHTTPAVVSHRAPVT----- 492
Db 472 GERSEYVTALEFDSPYKVMVIMETSHLYLFTETVGLTETETAPLEMYN PTTILREL 529
QY 493 QARE-----GNLPL--LIAPALAAVLLAALAAVCAAYCVPRGPAMAA-AAQHKQD 539
Db 530 QEKERYKNINLILAAITGGAAVALVTALLALV-CWYVHNGSLSEFEN-AYSKGR 582

RESULT 12
Q9NZU0 PRELIMINARY; PRT: 649 AA.
ID Q9NZU0;
AC Q9NZU0;
DT 01-OCT-2000 (TREMBLrel 15, Created)
DT 01-OCT-2000 (TREMBLrel 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel 19, Last annotation update)
DE LECICINE-RICH REPEAT TRANSMEMBRANE PROTEIN FLRT3 (D3581113.1).
GN FLRT3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN 11
RP SEQUENCE FROM N.A.
RX MEDLINE=20112755; PubMed 10644439;
RA Cary, S. E., Rana-Sabo, C. S., Rana, J. A., Forks, J. H.;
RT Identification of FLRT1, FLRT2, and FLRT3; A Novel Family of
RT Transmembrane Leucine-Rich Repeat Proteins.*;
PL ENA Acc. 1:R50490.1; FN_111.
DR InterPro: IPR001611; LRR.
DR InterPro: IPR000483; LRR_Gterm.
DR InterPro: IPR000372; LRR_Nterm.
DR InterPro: IPR003592; LRR_out.
DR InterPro: IPR003591; LRR_typ.
DR InterPro: IPR001211; PLP_A2.
DR Pfam: PF00041; fn3; 1.
DR Pfam: PF00560; LRR; 10.
DR Pfam: PF01463; LRRCT; 1.
DR Pfam: PF01462; LRRNT; 1.
DR SMART: SM00060; FN3; 1.
DR SMART: SM00370; LRR; 1.
DR SMART: SM00082; LRRCT; 1.
DR SMART: SM00013; LRRNT; 1.
DR SMART: SM00369; LRR_TYP; 1.

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RP SEQUENCE FROM N.A.
RA Isoqai T., Ota T., Hayashi Y., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nishikawa T., Nishikawa T., Nishikawa T., Nishikawa T.,
FA Matsukawa H., Ishii S., Fudai Y., Saito F., Yamamoto T., Wakabayashi A.,
RA Nakamura Y., Nakahara K., Masuko Y., Sasaki N.,
RT "NEDO human cDNA sequencing project";
RL Submitted (MAY 2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK027694; BAB5303.1; - P348057P107A7A CPO64;
SQ SEQUENCE 624 AA: 70245 MW: 74132 MW: 37981820407H01C0 CPO64;

Query Match          9.68; Score 299.5; DR 6; Length 677;
Best Local Similarity 24.28; Pred. No. 2,46-13;
Matches 140; Conservative 93; Mismatches 209; Indels 175; Gaps 25;

QY 22 QVPSGQVQSGQVETATQVTTVERIVPPVTGTVVFPNCITIMIDASSPACLP----- 77
DB 3 KSCPSSVGR-LAEFIYVGNRFETISPTIPEDATTIVYNNGL-----NNAQIPSELKN 55
78 -----LQILDLSQNIASH-----KPKKLLLLSHNSL- 106
DB 56 LUKVERIYLYHNSIDREPTNIPKYVRELUHGNNTPTIYDSLSKPIYLELHLDNVS 115
QY 107 -LAIPTCILPTANVALEPLACIGLGLDEGLFSEPIREHELVSDNGLTEK-LIVIKELR 164
DB 116 AVSLEGAERGSNY--LRGLFSLSNHSLI-LWGLPPIIFLPLILKPLISLSSSLAGLI 173
QY 165 GLTRPLACN-----TPIAQLP-----PPIAQLG----- 187
DB 174 SLKPIVLGNTINNGIGKGVFNVLNLTSLSVNSLTAAPVNLPGTINLKKLYLQNH 233
QY 188 LAAGLLGVNLSGALFGDLSGLTFLRLILAAAPNPNVCPPLSWPQFW 247
DB 234 NPVPNAPSYIPCTYPLMSNNLSNIPGTFEDLPNTQLILNNWYVYVPMKWVQW 243
QY 238 VFPSSHVTIASPPTCHPTPNACPLLELDYADEGCAITITIAVITIEVVKEPIALS 297
DB 294 LQSLPKVQ-NVAGLGCQAFKVKMAIKDAELFKCKISIVSLQI-----IATP 345
QY 298 SSLAPITLSPTAPATAPASPTAPPTGVPVPGQCPPEPTCIINSGTTHGCTHHILACT 357
DB 346 NIVYPAQGWAPVTKQED-----TFNPK-----ITKH----- 374
QY 358 PPGFTGIVQFSQMGCTPSPPTPTTPRPPSTTGIFVSPSTLPVGLQVYQSSVCLP 417
DB 375 -----QTTGSPS-----PKTITTVKSVTSNTTHISWKLALPWTALPLS 413
QY 418 SLPIITYPNISQD-DREIVTIPASIAATYVTQIPNNATYSVCMPLQCPGVCECEP--A 474
DB 414 WLKLGHSAPAGSITPTVT-----GPFSEYIVTAIFPSPYKVVWVPMTSNILYFETPV 459
QY 475 GPEHTPPAVHSHNAPVT-----QAPR-----LAFALAAVLLAALAAVGAAYC 523
DB 470 CTFETETAPILMN--PTTINRQFKFPEKPNIPILAAIGTAVAILVIAILVIAIV-TWVV 526
QY 524 VARGRAMAA AAOQKQ 539
DB 527 HNGSLSPNCAYSKGP 543

RESULT 15
Q24256 PRELIMINARY; PRT: 677 AA.
AC Q24256;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-AUG-1998 (Tremblrel. 07, last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, last annotation update)
DE GLYCOPROTEIN 1B.
OS Canis familiaris (Dog).
OC Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
OC Mammalia, Eutheria, Carnivora, Fissipedia, Canidae; Canis.
OX NCBI_TaxID=9615;
RN 11

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RP SEQUENCE FROM N.A.
FX MERLINE 20011007; Pubmed 10544923;
FA Kohny D., Metatsek P.A., Fahs S.A., Wallner D.C., Montgomery P.R.;
FI "Cloning and expression of canine glycoprotein 1balpha.";
RL Thromb. Haemost. 82:1327-1333(1999).
DR EMBL; U19489; AAC14361.1; -
DB 107-EPITOP; IPR001611; IPR_
DB 107-EPITOP; IPR000483; IPR_Cterm.
DB 107-EPITOP; IPR000370; IPR_Nterm.
DB 107-EPITOP; IPR003592; IPR_out.
DB 107-EPITOP; IPR003591; IPR_type.
DB Pfam; PF01463; LRRCT; 1.
DB Pfam; PF01462; LRRRT; 1.
DB SMART; SM00370; LRR; 2.
DB SMART; SM00082; LRRCT; 1.
DB SMART; SM00013; LRRNT; 1.
DB SMART; SM00359; LRR_type; 3.
SQ SEQUENCE 677 AA: 74132 MW: 37981820407H01C0 CPO64;

Query Match          9.68; Score 299.5; DR 6; Length 677;
Best Local Similarity 24.28; Pred. No. 2,46-13;
Matches 150; Conservative 90; Mismatches 189; Indels 221; Gaps 26;

QY 7 LLLPILLILLALPQVQGPSSNQVSLQVIVETAKQCTIVPRVPPVPTVGLYVFEN----- 62
DB 3 LLLWLLLLALPQPEPFCEVSFVTSQVE-VNCDNFGKALPPGIPGDTAILHLAENPLGA 61
QY 63 -----GIIIMIDASSFAGLQGLQILDLSQNIASH-----RIPRL 97
DB 62 FSTATIGELTFLALHILFESQITGLQVGM-----LPELELDVSHRKKASQISLGRALFAT 119
QY 98 LLDLHNSLLALPSTIITANVALEPLACIGLGLDEGLFSEPIREHELVSDNGLTEK 157
DB 120 TLDASERELVALSEGLD-----GLSGLHLLVLSGRKATLP 156
QY 158 P-VIVGSLKGIIFPLAGNIPILAQIPPELACIAALQPLDVSNI SLGAI P-----GHVSGIF 212
DB 157 PLLAFIACLEKLNLAUN-PLLELPFSELESLGLTLYLGNNIPVPGKGFLLIIP 215
QY 213 PLELLAAAPNPNVCPPLSWPQWVP-----PSHVTIASPPTCHPTPNACPLLELDY 255
DB 216 TPLH-----GNWSQCPCTIYIAFWPUNSNVVIWPCVFAKATPNSVSPVWKNV 270
QY 256 P-----PKNAGPILLLELDVADP-----GCPATTTTATV----- 283
DB 271 PVHTYQCDCTSPDQ-----DMVDYDREDEKLPCVEADATPAVVSFSLHKAHTHW 326
QY 284 -----PTTPTSTPTTQPPATTTTQPPATTT-----PTTPVVPPEPTALSSSLAPTW 405
DB 327 GLYPTFAVGHQMAVLSSTLELTKQCTMPDSTLQPMITTP-----EPTTFTTPTT 392
QY 406 SPVATAPSPSPSLAPVIVGVVQVQGLAPVSTQINAGCTHATTHHHACLPDSFTGLY 365
DB 363 TPTTP EPTTPTTPTTPTTPTT TPTTPTTPTTPTT-----TPTTPT----- 424
QY 366 QFSQMGCTPSPPTPTTPRPPSTTGIFVSPSTLPVGLQVYQSSVCLP 425
DB 425 -----PTTPTSTPTTQPPATTTTQPPATTT-----TQVATPTTPTTQ 464
QY 426 LSPHKEIVTILHLSIAIVIV-----LQEPATYVSVVMPGCPGR 471
DB 465 TTP--TTPPTPTTPTTPTTPTTPTT-----PTSPITTLHLSRNTPLIGPEL 516
QY 472 PEACCEAHTPPAVHSHNAP 490
DB 517 TSPCTTSEYIPVPSLVHLP 535

Search completed: September 17, 2002, 09:54:24
Job time: 260 sec

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